

QY 61 AAGTGTGGACAA 74
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 Db 295 AAGTGTGGACAA 308

RESULT 2
 BF840993/c 447 bp mRNA linear EST 13-JAN-2001
 LOCUS RC3-HT0974-011200-013-803 HT0974 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF840993
 ACCSSION BF840993
 VERSION BF840993.1 GI:12193641
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 447)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3kt2-RC3-HT0974-
 011200-013-803&f3=2000-12-01&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 29
 High quality sequence stop: 447.
 Location/Qualifiers

FEATURES
 source

1..447
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 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_id="HT0974"
 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI: A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 100.0%; Score 74; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 6.7e-16;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAAGGGGAACTTAGAGTTGTCATCATCGAGCCCTGTTTAGCTCAGATTCCG 60
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 Db 268 ATGCCAAGGGGAACTTAGAGTTGTCATCATCGAGCCCTGTTTAGCTCAGATTCCG 209
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 QY 61 AAGTGTGGACAA 74
 |||||
 Db 208 AAGTGTGGACAA 195

RESULT 3

AL702133 513 bp mRNA linear EST 04-SEP-2003
 LOCUS DKFZp686G02155.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DKFZp686G02155.5, mRNA sequence.
 AL702133
 ACCSSION AL702133
 VERSION AL702133.1 GI:19685488
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 513)
 Bloeker,H., Bocher,M., Brandt,P., Mewes,W., Well,B. and
 Wiemann,S.
 EST (Bloeker,H., Bocher,M., Brandt,P., Mewes,W., Well,B. and
 Wiemann,S.)
 Unpublished (1999)
 CONTACT: MIPS

COMMENT MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GfR (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No sl sequence available.
 This clone (DKFZp686G02155) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
 Location/Qualifiers

FEATURES
 source

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 /mol_type="mRNA"
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 /clone="DKFZp686G02155"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_id="686 (synonym: hlcc3)"
 /note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI;
 cDNA-collection"

ORIGIN

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 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 343 ATGCCAAGGGGAACTTAGAGTTGTCATCATCGAGCCCTGTTTAGCTCAGATTCCG 402
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 QY 61 AAGTGTGGACAA 74
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 Db 403 AAGTGTGGACAA 416

RESULT 4

BP243833 580 bp mRNA linear EST 15-SEP-2004
 LOCUS BP243833 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
 DEFINITION BP243833
 ACCSSION BP243833
 VERSION BP243833.1 GI:52116743
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 580)
 Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	100.0	117	13	US-10-050-189A-10	Sequence 10, Apr
2	74	100.0	4256	20	US-10-719-993-319	Sequence 319, Apr
3	74	100.0	4803	10	US-09-930-213-276	Sequence 276, Apr
4	74	100.0	4803	21	US-10-956-157-1094	Sequence 1094, Apr
5	74	100.0	5840	20	US-10-719-993-322	Sequence 322, Apr
6	74	100.0	5924	13	US-10-041-886-2	Sequence 2, Apr
7	74	100.0	5957	20	US-10-719-993-330	Sequence 330, Apr

C 8	74	100.0	6107	20	US-10-719-993-321	Sequence 321, App
C 9	74	100.0	6179	20	US-10-719-993-318	Sequence 318, App
C 10	74	100.0	65479	13	US-10-041-856-1	Sequence 1, Appl
C 11	74	100.0	78878	20	US-10-719-993-6863	Sequence 6863, Ap
C 12	57	77.0	201	20	US-10-719-993-34499	Sequence 4499, Ap
C 13	57	77.0	201	20	US-10-719-993-4457	Sequence 4527, Ap
C 14	57	77.0	201	20	US-10-719-993-4456	Sequence 4556, Ap
C 15	57	77.0	201	20	US-10-719-993-4585	Sequence 4585, Ap
C 16	57	77.0	201	20	US-10-719-993-4613	Sequence 4613, Ap
C 17	27.6	37.3	1899	17	US-10-282-1228-24563	Sequence 24563, A
C 18	27	36.5	201	20	US-10-719-993-34903	Sequence 34903, A
C 19	26.6	35.9	941	13	US-10-005-0578-38	Sequence 38, Appl
C 20	26.6	35.9	941	18	US-10-675-0728-5	Sequence 5, Appl
C 21	26.4	35.7	1855	19	US-10-437-963-100577	Sequence 100577,
C 22	26.4	35.7	4320	19	US-10-630-518-17	Sequence 17, Appl
C 23	26.4	35.7	4320	20	US-10-630-518-21	Sequence 21, Appl
C 24	26	35.1	2920	20	US-10-739-930-898	Sequence 898, Appl
C 25	25.8	34.9	1600	22	US-10-972-079-67653	Sequence 76053, A
C 26	25.8	34.9	1563	9	US-09-938-8428-672	Sequence 672, App
C 27	25.8	34.9	1563	11	US-09-938-8428-672	Sequence 672, App
C 28	25.6	34.6	201	20	US-10-719-993-52377	Sequence 52377, A
C 29	25.6	34.6	484	19	US-10-437-963-63832	Sequence 63832, A
C 30	25.6	34.6	186854	21	US-10-872-156-34	Sequence 34, Appl
C 31	25.6	34.6	248436	13	US-10-087-192-2014	Sequence 2014, Ap
C 32	25.6	34.6	330926	20	US-10-719-993-7048	Sequence 7048, Ap
C 33	25.4	34.3	936289	19	US-10-922-281-21	Sequence 21, App
C 34	25.2	34.1	535	20	US-10-363-3458-33723	Sequence 33723, A
C 35	25.2	34.1	535	20	US-10-363-3458-33724	Sequence 33724, A
C 36	25.2	34.1	535	21	US-10-363-4838-33723	Sequence 32723, A
C 37	25.2	34.1	535	21	US-10-363-4838-33724	Sequence 32724, A
C 38	25.2	34.1	617	13	US-10-027-632-244158	Sequence 244158, Sequence 244158,
C 39	25.2	34.1	617	17	US-10-027-632-244158	Sequence 244158,
C 40	25.2	34.1	3186778	13	US-10-027-632-114961	Sequence 114961,
C 41	25.2	34.1	3186778	17	US-10-027-632-114961	Sequence 114961,
C 42	25	33.8	981	10	US-09-822-846-283	Sequence 282, App
C 43	25	33.8	1811	10	US-09-822-846-283	Sequence 283, App
C 44	25	33.8	2666	20	US-10-425-115-51127	Sequence 51127, A
C 45	24.8	33.5	600	22	US-10-972-079-35597	Sequence 35597, A

ALIGNMENTS

```

RESULT 1
US-10-050-189A-10
: Sequence 10. Application US/10050189A
: Publication No. US20020168656A1
: GENERAL INFORMATION:
: APPLICANT: Rubin, Berish
: APPLICANT: Anderson, Sylvia
: TITLE OF INVENTION: Detection of Mutations in a Gene Encoding IKB Kinase-Complex-Associated Protein to Diagnose Familial Dysautonomia
: FILE REFERENCE: Rubin 201
: CURRENT APPLICATION NUMBER: US/10/050.189A
: CURRENT FILING DATE: 2002-01-16
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 10
: LENGTH: 117
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-050-189A-10

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Db	28	ATGCCAAGGGGAAACTTAGAAGTTCATCATCATGAGCCCTGTTTAAAGTCACAGATTGG	87	
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Db 88 AAGTGGTTGACAA 101

RESULT 2

US-10-719-993-319
; Sequence 319, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 4256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-319

Query Match 100.0%; Score 74; DB 20; Length 4256;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 60

Db 2491 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 2550

QY 61 AAGTGGTTGACAA 74

Db 2551 AAGTGGTTGACAA 2564

RESULT 3

US-09-930-213-276
; Sequence 276, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAEFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHER-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELMELGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 276
; LENGTH: 4803
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-213-276

Query Match 100.0%; Score 74; DB 10; Length 4803;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 60

Db 2434 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 2493

QY 61 AAGTGGTTGACAA 74

Db 2494 AAGTGGTTGACAA 2507

RESULT 4

US-10-956-157-1094
; Sequence 1094, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Myelch
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 1094
; LENGTH: 4803
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-1094

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Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2434 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 2493

QY 61 AAGTGGTTGACAA 74

Db 2494 AAGTGGTTGACAA 2507

RESULT 5

US-10-719-993-322
; Sequence 322, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 5840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-322

Query Match 100.0%; Score 74; DB 20; Length 5840;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 60

Db 2491 ATGCCAAGGGGAAACTTAGAAGTTGTCATCATCGAGCCCTGGTTTAACTCAGATTCCG 2550

QY 61 AAGTGGTTGACAA 74

Db 2551 AAGTGGTTGACAA 2564

RESULT 6

US-10-041-856-2
; Sequence 2, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:44:02 ; Search time 2130.01 Seconds
(without alignments)
1683.411 Million cell updates/sec

Title: US-10-041-856-2_COPY_2441_2514

Perfect score: 74
Sequence: 1 atgcgaagggaactaga.....atccgaagctgtgcacaa 74

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	117	6	AX481363 Sequence
2	74	100.0	803	6	BD147310 Primer fo
3	74	100.0	803	6	AX867248 Sequence
4	74	100.0	2471	6	BD157787 Primer fo
5	74	100.0	2471	6	AX879348 Sequence
6	74	100.0	2471	9	AK022559 Homo sapi
7	74	100.0	3516	6	CO724004 Sequence
8	74	100.0	3999	6	AR070165 Sequence
9	74	100.0	3999	6	AR124807 Sequence
10	74	100.0	4417	6	CQ850139 Sequence
11	74	100.0	4417	9	AK127237 Homo sapi
12	74	100.0	4788	6	BD156525 Sequence
13	74	100.0	4788	6	AX877177 Sequence
14	74	100.0	4788	9	AK001641 Homo sapi
15	74	100.0	4803	6	BD171366 Method fo
16	74	100.0	4803	6	BD173600 Method of
17	74	100.0	4803	6	AX210634 Sequence
18	74	100.0	4803	9	AF044195 Homo sapi
19	74	100.0	5047	9	BC033094 Homo sapi

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22	74	100.0	66479	6	AX676048 Sequence
23	74	100.0	78376	9	AL355962 Human DNA
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26	59.6	80.5	4765	10	BC053287 Mus muscu
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28	59.6	80.5	5011	10	AF140786 Mus muscu
29	59.6	80.5	5034	10	AF387811 Mus muscu
30	59.6	80.5	224915	2	AC096902 Rattus no
31	59.6	80.5	264321	10	AL807762 Mouse DNA
32	50.6	48.4	4169	5	AJ720452 Gallus ga
33	35.8	48.4	128177	2	EX927373 Datio rer
34	30.8	41.6	160516	10	AL928943 Mouse DNA
35	29.2	39.5	2535	3	AK173465 Ciona int
36	29	39.2	68661	3	AC024805 Caenorhab
37	29	39.2	278007	2	AC006799 Caenorhab
38	28.2	38.1	181585	9	AL139350 Human DNA
39	27.8	37.6	181644	9	AC104989 Homo sapi
40	27.6	37.3	8868	3	CEY32812A Caenorhab
41	27.6	37.3	222204	2	AC126953 Rattus no
42	27.6	37.3	224499	14	AF482758 Compox vi
43	27.6	37.3	324050	1	AL591983 Listeria
44	27.6	37.3	349980	6	AX641671 Sequence
45	27.6	37.3	349980	6	AX641672 Sequence

ALIGNMENTS

RESULT 1	AX481363	Sequence 10 from Patent EP12523232.	117 bp	DNA	linear	PAT 16-AUG-2002
LOCUS	AX481363					
DEFINITION	Sequence 10 from Patent EP12523232.					
ACCESSION	AX481363					
VERSION	AX481363.1	GI:22316264				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE						
AUTHORS	Rubin, B.Y. and Anderson, S.L.					
TITLE	Detection of mutations in a gene encoding 1kappab					
JOURNAL	Kinase-complex-associated protein to diagnose familial dysautonomia					
PATENT	Patent: EP 125232-A 10 24-JUL-2002;					
Rubin, Berish Y. (US) ; Anderson, Silvia L. (US)						
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QY	1	ATGCCAAGGGAACCTTAGAGTTCATCATCGAGCCCTGTTTACGCTCAGATTGGG	60			
DB	28	ATGCCAAGGGAACCTTAGAGTTCATCATCGAGCCCTGTTTACGCTCAGATTGGG	87			
OY	61	AAGTGTGACAA	74			
DB	88	AAGTGTGACAA	101			
RESULT 2	BD147310	803 bp	DNA	linear	PAT 17-JAN-2003	
LOCUS	BD147310					
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.					
ACCESSION	BD147310					

VERSION BD147310.1 GI:27853068
KEYWORDS JP 2002191363-A/2153.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Euteria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 803)
Ota,T., Isogai,T., Nishikawa,T., Hayaashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 2153 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/2153
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10', C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT source 1..803
FT /organism='Homo sapiens (human)'.
FEATURES
source 1..803
/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 74; DB 6; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAACTCAGATTCCG 60
Db 123 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAACTCAGATTCCG 182
Qy 61 AAGTGGTTGACAA 74
Db 183 AAGTGGTTGACAA 196
RESULT 3
AX867248
LOCUS AX867248 803 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 2153 from Patent EP1074617.
ACCESSION AX867248
VERSION AX867248.1 GI:40021619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
1
Ota,T., Isogai,T., Nishikawa,T., Hayaashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 2153 07-FEB-2001;
Research Association for Biotechnology (JP)
Location/Qualifiers
FEATURES
source 1..803
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 74; DB 6; Length 803;

Best Local Similarity 100.0%; Pred. No. 1.8e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAACTCAGATTCCG 60
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Qy 61 AAGTGGTTGACAA 74
Db 183 AAGTGGTTGACAA 196
RESULT 4
BD157787
LOCUS BD157787 2471 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD157787
VERSION BD157787.1 GI:27863545
KEYWORDS JP 2002191363-A/12630.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2471)
Ota,T., Isogai,T., Nishikawa,T., Hayaashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 12630 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/12630
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10', C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (772)..(1989).
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source 1..2471
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAACTCAGATTCCG 60
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Qy 61 AAGTGGTTGACAA 74
Db 183 AAGTGGTTGACAA 196
RESULT 5
AX879348
LOCUS AX879348 2471 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 14253 from Patent EP1074617.
ACCESSION AX879348
VERSION AX879348.1 GI:40034084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 09:42:59 ; Search time 523.938 Seconds
(without alignments)
836.092 Million cell updates/sec

Title: US-10-041-856-2_COPY_2441_2514

Perfect score: 74

Sequence: 1 atgcgaaggaggaaactcaga.....atccgaagctggtgcacaa 74

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	74	100.0	2471	4	AaH15795 Human CDN
4	74	100.0	3999	2	AaX28025 Human IKA
5	74	100.0	3999	4	AaF29756 Human IKA
6	74	100.0	4417	13	ADR07102 Full leng
7	74	100.0	4788	4	AaH14533 Human CDN
8	74	100.0	4803	5	AaH81767 Human dif
9	74	100.0	4803	6	AaL44190 Human I-k
10	74	100.0	5924	6	ABO80570 Mutant hu
11	74	100.0	5924	6	ABO80569 Human IKB
12	74	100.0	5924	8	ACD13384 Human DNA
13	74	100.0	66479	6	ABO80567 Mutant hu
14	74	100.0	66479	6	ABO80566 Mutant hu
15	74	100.0	66479	6	ABO80568 Mutant hu
16	74	100.0	66479	6	ABO80565 Human IKB
17	59.6	80.5	4645	8	ABD53601 Primary r
18	27.6	37.3	11899	8	ACA36693 Prokaryot
19	27.6	37.3	110000	6	ABA03041_23 Continuation (24 o
20	27.6	37.3	110000	6	ABA03041_24 Continuation (25 o

21	26.6	35.9	941	6	ABO75916
22	26.4	35.7	4320	6	AaL48977
23	25.8	34.9	1008	10	ABD50065
24	25.8	34.9	1563	3	AaC43257
25	25.8	34.9	1563	6	ABZ12867
26	25.8	34.9	1563	6	ADG87872
27	25.8	34.9	1563	6	ADG88134
28	25.8	34.9	2252	4	ABL21828
29	25.8	34.9	2384	4	ABL21864
30	25.6	34.6	24636	11	ACN45190
31	25.4	34.3	792	4	ABL16845
32	25.4	34.3	2792	4	ABL16844
33	25.4	34.3	5106	4	ABL08100
34	25.4	34.3	96289	13	ABD33205
35	25.4	34.3	110000	6	ABA90521_21
36	25.2	34.1	535	6	ABO46132
37	25.2	34.1	535	6	ABO46133
38	25.2	34.1	5623	4	ABL18300
39	25	33.8	981	6	ABK35891
40	25	33.8	1811	6	ABK35892
41	25	33.8	3474	12	ADQ62997
42	25	33.8	109973	3	AAE22298
43	24.8	33.5	1244	4	AAH73111
44	24.8	33.5	1244	4	AAH73113
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ALIGNMENTS

RESULT 1

ID ABN84790 standard; CDNA; 117 BP.

AC ABN84790;

DT 05-NOV-2002 (first entry)

DE Ikappab kinase-complex-associated protein exon 19-21 sequence.

XX Familial dysautonomia; Riley-Day syndrome;

KW hereditary sensory neuropathy II; human; carrier; diagnosis;

KW Ikappab kinase-complex associated protein; IKA; chromosome 9q31; gene;

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..117

FT /tag= a

FT /product= "IKAP peptide"

FT /notes= "the CDS does not include a start or stop codon"

FT EPI225232-A2.

FT 24-JUL-2002.

FT 17-JAN-2002; 2002EP-00001232.

FT 17-JAN-2001; 2001US-0262884P.

XX (RUBI/) RUBIN B. Y.

XX (ANDE/) ANDERSON S. L.

XX Rubin BY, Anderson SL;

DR MPI; 2002-601228/65.

DR P-PSDB; ABB79767.

PT Detecting a polymorphism in a gene encoding the Ikappab kinase-complex-

PT associated protein is used to diagnose and identify carriers of familial

PT dysautonomia.

XX Disclosure; Fig 1B; 16pp; English.
PS
XX The present sequence comprises cDNA corresponding to exons 19-21 of the
CC IkarpB kinase complex-associated protein (IKAP) gene of an individual
CC unaffected by familial dysautonomia (FD). It was obtained by PCR
CC amplification using the primers given in ABN84788-89. Alignment of this
CC sequence with that from an FD-affected individual (see ABN84791)
CC indicated that exclusion of exon 20 in the RNA transcribed from the FD
CC allele resulted in a frameshift, causing premature termination of
CC translation and a protein truncated by 619 amino acids. Normal IKAP has
CC 1332 amino acids. The invention provides a method for detecting a
CC polymorphism linked to a gene associated with FD. This allows the
CC diagnosis of FD and the identification of carriers. It involves detecting
CC a disruptive mutation in a gene encoding IKAP on chromosome 9q31. The
CC mutation is a T to C transition in position 6 of the donor splice site of
CC intron 20 and/or a G to C transversion of nucleotide 2390 in exon 19 of
CC the IKAP gene
XX
SQ Sequence 117 BP; 35 A; 22 C; 29 G; 31 T; 0 U; 0 Other;
Query Match 100.0%; Score 74; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.2e-18;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAGCTCAGATTCCG 60
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QY 61 AAGTGTGGACAA 74
Db 88 AAGTGTGGACAA 101
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XX
AC AAH05318;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:2153.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-00116126.
XX
PF 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
PS Claim 1; SEQ ID NO 2153; 2537bp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification, where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the 5602
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;
Query Match 100.0%; Score 74; DB 4; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAGCTCAGATTCCG 60
Db 123 ATGCCAAGGGGAACTTAGAAGTTGTCATCATCGAGCCCTGTTTAGCTCAGATTCCG 182
QY 61 AAGTGTGGACAA 74
Db 183 AAGTGTGGACAA 196
RESULT 3
ID AAH15795 standard; cDNA; 2471 BP.
XX
AC AAH15795;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14253.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-00116126.
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PF 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:57:07 ; Search time 153.025 Seconds
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791.274 Million cell updates/sec

Title: US-10-041-856-2_COPY_2441_2514

Perfect score: 74

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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13	24.2	32.7	8021	3 US-09-740-235-2	Sequence 2, Appli
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15	24	32.4	2412	4 US-09-583-110-553	Sequence 553, App
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42	23.2	31.4	601	4 US-09-949-016-86782	Sequence 86782, A
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45	23.2	31.4	2967	3 US-08-637-823B-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-08-971-244-1
Sequence 1, Application US/08971244
Patent No. 5891719
GENERAL INFORMATION:
APPLICANT: Cohen, Lucy
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,244
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3996
US-08-971-244-1
Query Match 100.0%; Score 74; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred. No. 2,7e-19;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2131 ATGCCAAGGGGAACTTAGAAGTTTCATCATCGAGCCCTGGTTTACCTCAGATTCCG 2190
QY 61 |||||
Db 2191 AAGTGTGGACAA 2204

RESULT 2

US-09-286-891-1
Sequence 1, Application US/09286891
Patent No. 612195

GENERAL INFORMATION:
APPLICANT: Cohen, Lucy

APPLICANT: Baerzle, Patrick

TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: 2

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/286,891

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,244

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-011

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3999 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3996

US-09-286-891-1

Query Match 100.0%; Score 74; DB 3; Length 3999;
Best Local Similarity 100.0%; Pred. No. 2,7e-19;

Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAAGGGGAACTTAGAAGTTTCATCATCGAGCCCTGGTTTACCTCAGATTCCG 60
Db 2131 ATGCCAAGGGGAACTTAGAAGTTTCATCATCGAGCCCTGGTTTACCTCAGATTCCG 2190
QY 61 AAGTGTGGACAA 74
Db 2191 AAGTGTGGACAA 2204

RESULT 3

US-09-949-016-13498/c

Sequence 13498, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13498
LENGTH: 343352
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(343352)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13498

Query Match 34.9%; Score 25.8; DB 4; Length 343352;
Best Local Similarity 63.9%; Pred. No. 32;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 8 GGGGAAGCTTGAAGTTTCATCATCGAGCCCTGGTTTACCTCAGATTCCGAGTGT 67
Db 11264 GTGGTAATGAAGCTGTGTATATGTCCTATATGTCATGTCAGATTGGGAAGTGT 11205
QY 68 T 68
Db 11204 T 11204

RESULT 4
US-09-949-016-124821/c
Sequence 124821, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124821
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-124821

Query Match 33.8%; Score 25; DB 4; Length 601;
Best Local Similarity 58.9%; Pred. No. 5.2;
Matches 43; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 TGGCAAGGGGAACTTAGAAGTTTCATCATCGAGCCCTGGTTTACCTCAGATTCCG 61
Db 586 TGCTAAGAGGAATTTCTAATGTTTCAACACAAACTATGATTAATTCAC 527
QY 62 AAGTGTGGACAA 74
Db 526 ATTGTAATTTAGAA 514

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 734.537 Seconds

(without alignments)
777.311 Million cell updates/sec

Title: US-10-041-856-85

Perfect score: 15

Sequence: 1 aagtaagagccatg 15

Scoring table: IDENTITY_NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.6	97.3	273	4	BG221595 RST41409
C 2	14.6	97.3	354	8	AQ168111 HS_2233_A
C 3	14.6	97.3	456	1	A1492486 C128E08_X
C 4	14.6	97.3	458	1	A1492495 C128F07_X
C 5	14.6	97.3	550	4	BM582147 170006872
C 6	14.6	97.3	668	5	BQ407386 GA_E010
C 7	14.6	97.3	679	5	BX113682 BX113682
C 8	14.6	97.3	737	9	CE603670 CIGR-gss-
C 9	14.6	97.3	749	9	CR337519 CGF100477
C 10	14.6	97.3	841	7	CN202392 Tor2548 G
C 11	14.6	97.3	848	2	BE570328 601333209
C 12	14.6	97.3	905	1	A1348093 QP61911.X
C 13	13.6	90.7	164	8	A2463592 IM0272801
C 14	13.6	90.7	235	1	AV033029 AV033029
C 15	13.6	90.7	252	2	BF773503 CM2-IT003
C 16	13.6	90.7	262	8	A2554007 RPT-23-2
C 17	13.6	90.7	280	4	BM570636 1104F01.Y
C 18	13.6	90.7	282	4	BG234760 dab63f11.
C 19	13.6	90.7	291	9	BX243232 Danto rer
C 20	13.6	90.7	304	6	CD410777 GM_CK308
C 21	13.6	90.7	319	8	A2234490 RPT-23-8
C 22	13.6	90.7	341	5	BY214916 BY214916
C 23	13.6	90.7	341	7	CK519547 rsw60_00
C 24	13.6	90.7	348	2	BE637256 WHE1295-1

C 25	13.6	90.7	351	5	BY324268 BY324268
C 26	13.6	90.7	360	8	A2768375 1M056813
C 27	13.6	90.7	360	9	CC592729 CH240_393
C 28	13.6	90.7	373	9	CR111055 Reverse 8
C 29	13.6	90.7	389	7	CK300936 U1-B-E01
C 30	13.6	90.7	392	4	B1750496 B1750496
C 31	13.6	90.7	404	8	A2231614 A2231614
C 32	13.6	90.7	410	9	CM524034 OP_Ba004
C 33	13.6	90.7	413	8	A0076964 CIT-HSP-2
C 34	13.6	90.7	431	8	A0518681 HS_5085-B
C 35	13.6	90.7	433	8	A2707731 RPT-23-2
C 36	13.6	90.7	446	2	BE845860 232684_BA
C 37	13.6	90.7	475	8	A2289694 RPT-23-1
C 38	13.6	90.7	482	6	CA590184 hab23a07.
C 39	13.6	90.7	496	4	BI449178 daa99h05.
C 40	13.6	90.7	503	2	AM603835 CM0-CNO4
C 41	13.6	90.7	511	1	AL693507 AL693507
C 42	13.6	90.7	518	1	AL694388 AL694388
C 43	13.6	90.7	519	7	CF799849 Lr_PAHCF
C 44	13.6	90.7	521	8	A2237823 RPT-23-7
C 45	13.6	90.7	525	2	AM169454 xj28e07.x

ALIGNMENTS

RESULT 1
BG221595/c 273 bp mRNA linear EST 21-APR-2001
LOCUS RST41409 Atherys RAGE Library Homo sapiens CDNA, mRNA sequence.
DEFINITION BG221595
ACCESSION BG221595
VERSION BG221595.1 GI:13747616
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 273)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozery,S.,
Mays,R., Smith,E., Veloso,N., Kliska,A., Hees,J., Colhoun,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atherys.com
High quality sequence stop: 223.
location/Qualifiers
1..273
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Atherys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology', in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 97.3%; Score 14.6; DB 4; Length 273;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
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Db 52 AAGTAAGGCCATTG 38

RESULT 2
LOCUS A0168111
DEFINITION HS 2233 A1 F07 MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=13 Row=K, genomic survey

ACCESSION A0168111 354 bp DNA linear GSS 16-OCT-1998
VERSION A0168111
KEYWORDS A0168111.1 GI:3561746
SOURCE GSS.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 354)
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2233 row: K column: 13
Class: BAC ends
High quality sequence stop: 354.
Location/Qualifiers
1..354
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2233 Col=13 Row=K"
/sex="male"
/clone_1b="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 97.3%; Score 14.6; DB 8; Length 354;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
|||||:|||||
Db 262 AAGTAAGGCCATTG 276

RESULT 3
LOCUS A1492486/c
DEFINITION c128608.x1 NCI CGAP K1d11 Homo sapiens CDNA clone IMAGE:2131814 3' similar to contains_MER7.t3 MER7 repetitive element ;, mRNA
sequence.
A1492486 456 bp mRNA linear EST 30-MAR-1999
A1492486 GI:4393489
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 456)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-dio.lnl.gov/bbrp/image/image.html
Insert length: 771 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
Location/Qualifiers
1..456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2131814"
/lab_host="DH10B"
/clone_1b="NCI CGAP K1d11"
/note="Organ: kidney; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP K1d11 was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Facina Bonaudo."

ORIGIN
Query Match 97.3%; Score 14.6; DB 1; Length 456;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
|||||:|||||
Db 271 AAGTAAGGCCATTG 257

RESULT 4
LOCUS A1492495/c
DEFINITION c128607.x1 NCI CGAP K1d11 Homo sapiens CDNA clone IMAGE:2131813 3' similar to contains_MER7.t3 MER7 repetitive element ;, mRNA
sequence.
A1492495 458 bp mRNA linear EST 30-MAR-1999
A1492495 GI:4393498
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 458)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:57:07 ; Search time 31.0185 Seconds

(without alignments)
791.274 Million cell updates/sec

Title: US-10-041-856-85

Perfect score: 15

Sequence: 1 aagtaagcgcatcg 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCUTS.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	14.6	97.3	246240	2	US-08-724-394A-22
4	13.6	90.7	390	4	US-09-134-000C-1436
5	13.6	90.7	430	3	US-09-280-116-233
6	13.6	90.7	601	4	US-09-949-016-34133
7	13.6	90.7	601	4	US-09-949-016-85899
8	13.6	90.7	601	4	US-09-949-016-130381
9	13.6	90.7	1020	3	US-08-913-264-3
10	13.6	90.7	3260	3	US-08-913-264-12
11	13.6	90.7	3105	4	US-09-543-681A-4000
12	13.6	90.7	7355	4	US-09-900-920-1
13	13.6	90.7	13417	2	US-08-637-759B-37
14	13.6	90.7	13417	3	US-08-871-355A-37
15	13.6	90.7	13417	3	US-09-201-945-37
16	13.6	90.7	50000	3	US-09-146-053-3
17	13.6	90.7	56694	4	US-09-949-016-12568
18	13.6	90.7	56702	4	US-09-949-016-15423
19	13.6	90.7	147382	4	US-09-949-016-14624
20	13.6	90.7	422592	4	US-09-949-016-14182
21	13.2	88.0	601	4	US-09-949-016-34134
22	13.2	88.0	601	4	US-09-949-016-130382
23	13.2	86.7	601	4	US-09-949-016-41948
24	13.2	86.7	601	4	US-09-949-016-57865
25	13.2	86.7	601	4	US-09-949-016-57866
26	13.2	86.7	601	4	US-09-949-016-78824
27	13.2	86.7	601	4	US-09-949-016-90072

28	13	86.7	601	4	US-09-949-016-90073	Sequence 90073, A
29	13	86.7	601	4	US-09-949-016-90074	Sequence 90074, A
30	13	86.7	601	4	US-09-949-016-120317	Sequence 120317, A
31	13	86.7	601	4	US-09-949-016-120318	Sequence 120318, A
32	13	86.7	601	4	US-09-949-016-123965	Sequence 123965, A
33	13	86.7	601	4	US-09-949-016-171546	Sequence 171546, A
34	13	86.7	601	4	US-09-949-016-199187	Sequence 199187, A
35	13	86.7	614	3	US-09-280-116-71	Sequence 71, Appl
36	13	86.7	747	4	US-08-956-171E-650	Sequence 650, App
37	13	86.7	747	4	US-08-781-986A-650	Sequence 650, App
38	13	86.7	918	3	US-09-134-001C-2201	Sequence 2201, App
39	13	86.7	918	4	US-09-711-164-223	Sequence 223, App
40	13	86.7	1001	4	US-09-671-317-424	Sequence 424, App
41	13	86.7	1470	4	US-09-328-352-1204	Sequence 1204, App
42	13	86.7	1555	3	US-08-747-574-3	Sequence 3, Appli
43	13	86.7	1615	4	US-09-820-002-1	Sequence 1, Appli
44	13	86.7	1638	4	US-09-949-016-5675	Sequence 5675, App
45	13	86.7	1683	4	US-09-248-796A-8877	Sequence 8877, App

ALIGNMENTS

RESULT 1
US-08-724-394A-20/C
Sequence 20 Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Laufer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolfe, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fites, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURES:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note="HLA-H.CONTIG"
US-08-724-394A-20

Query Match 97.3%; Score 14.6; DB 2; Length 246240;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGYGCCTTG 15
DB 155908 AAGTAAGTGCCTTG 155894

RESULT 2

US-08-724-394A-21/C
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Laue, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filtz, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

Query Match 97.3%; Score 14.6; DB 2; Length 246240;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGYGCCTTG 15
DB 155908 AAGTAAGTGCCTTG 155894

RESULT 3
US-08-724-394A-22/C
Sequence 22, Application US/08724394A

Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Laue, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filtz, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match 97.3%; Score 14.6; DB 2; Length 246240;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGYGCCTTG 15
DB 155908 AAGTAAGTGCCTTG 155894

RESULT 4
US-09-134-000C-1436/C
Sequence 1436, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 1436

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: July 31, 2005, 16:38:33 ; Search time 153.148 Seconds
(without alignments)
633.931 Million cell updates/sec

Title: US-10-041-856-85

Perfect score: 15

Sequence: 1 aagtaagcgcattg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 22: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.6	97.3	15	US-10-041-856-85	Sequence 85, Appl1
2	14.6	97.3	201	US-10-719-993-34993	Sequence 34903, A
3	14.6	97.3	369	US-10-487-901-3816	Sequence 3816, Ap
4	14.6	97.3	593	US-10-487-901-4354	Sequence 4354, Ap
5	14.6	97.3	721	US-10-027-632-32790	Sequence 32790, A
6	14.6	97.3	721	US-10-027-632-32791	Sequence 32791, A
7	14.6	97.3	721	US-10-027-632-32790	Sequence 32790, A

Query Match	Score	DB	ID	Description	
8	14.6	97.3	721	US-10-027-632-32791	Sequence 32791, A
9	14.6	97.3	1139	US-10-437-963-67889	Sequence 67889, A
10	14.6	97.3	66479	US-10-041-856-1	Sequence 1, Appl1
11	14.6	97.3	78878	US-10-719-993-6863	Sequence 6863, Ap
12	14.6	97.3	235033	US-10-301-844-1	Sequence 1, Appl1
13	14.6	97.3	237326	US-10-301-844-2	Sequence 2, Appl1
14	13.6	90.7	25	US-10-956-157-17167	Sequence 17167, A
15	13.6	90.7	25	US-10-956-157-26777	Sequence 26777, A
16	13.6	90.7	25	US-10-956-157-26777	Sequence 26777, A
17	13.6	90.7	228	US-10-719-956-106967	Sequence 106967, A
18	13.6	90.7	228	US-10-398-221-776	Sequence 776, App
19	13.6	90.7	422	US-10-767-701-17492	Sequence 17492, A
20	13.6	90.7	541	US-10-027-632-115092	Sequence 115092, A
21	13.6	90.7	541	US-10-027-632-115093	Sequence 115093, A
22	13.6	90.7	541	US-10-027-632-115092	Sequence 115092, A
23	13.6	90.7	541	US-10-027-632-115092	Sequence 115092, A
24	13.6	90.7	541	US-10-027-632-115093	Sequence 115093, A
25	13.6	90.7	541	US-10-027-632-115094	Sequence 115094, A
26	13.6	90.7	570	US-10-425-115-116253	Sequence 116253, A
27	13.6	90.7	595	US-09-840-743-68	Sequence 68, Appl1
28	13.6	90.7	600	US-10-956-157-10380	Sequence 10380, A
29	13.6	90.7	600	US-10-972-079-28919	Sequence 28919, A
30	13.6	90.7	609	US-10-972-079-28919	Sequence 85665, A
31	13.6	90.7	609	US-10-027-632-85666	Sequence 85666, A
32	13.6	90.7	609	US-10-027-632-303182	Sequence 303182, A
33	13.6	90.7	609	US-10-027-632-85666	Sequence 85666, A
34	13.6	90.7	706	US-10-027-632-303182	Sequence 303182, A
35	13.6	90.7	751	US-10-437-963-35749	Sequence 35749, A
36	13.6	90.7	1305	US-10-437-963-2628	Sequence 7508, Ap
37	13.6	90.7	1305	US-10-437-963-2628	Sequence 2628, Ap
38	13.6	90.7	1446	US-10-425-115-177687	Sequence 177687, A
39	13.6	90.7	1452	US-09-070-9274-246	Sequence 246, Appl1
40	13.6	90.7	1592	US-10-425-115-177698	Sequence 177698, A
41	13.6	90.7	1953	US-10-956-157-5145	Sequence 5145, Ap
42	13.6	90.7	1957	US-09-864-761-16018	Sequence 16018, A
43	13.6	90.7	2162	US-10-684-129-25	Sequence 25, Appl1
44	13.6	90.7	2173	US-10-684-129-11	Sequence 11, Appl1
45	13.6	90.7	2175	US-10-684-129-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1

US-10-041-856-85

Sequence 85, Application US/10041856

Publication No. US20020169299A1

GENERAL INFORMATION:

APPLICANT: SLATGENHAUPT, SUSAN

INVENTOR: GUSELDA, JAMES P.

TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL

FILE REFERENCE: 1829-4004US1

CURRENT APPLICATION NUMBER: US/10/041,856

PRIOR FILING DATE: 2002-07-08

PRIOR APPLICATION NUMBER: 60/260,080

PRIOR FILING DATE: 2001-01-06

NUMBER OF SEQ ID NOS: 88

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 85

LENGTH: 15

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Probe

US-10-041-856-85

Query Match 97.3%; Score 14.6; DB 13; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAGTAAGGCCATTG 15

RESULT 2

US-10-719-993-34903
; Sequence 34903, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34903
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-34903

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
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Db 26 AAGTAAGGCCATTG 40

RESULT 3

US-10-487-901-3816/c
; Sequence 3816, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Meglarz, Thaddaus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentn version 3.1
; SEQ ID NO 3816
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Trichoderma harzianum
US-10-487-901-3816

Query Match 97.3%; Score 14.6; DB 21; Length 369;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
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Db 43 AAGTAAGGCCATTG 29

RESULT 4

US-10-487-901-4354/c
; Sequence 4354, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:

APPLICANT: Oreido, Jeremiah Vincent

APPLICANT: McCreery, David

APPLICANT: Pell, Randy

APPLICANT: Miller, Barbara

APPLICANT: Meglarz, Thaddaus

APPLICANT: Gachotte, Daniel

APPLICANT: Blakeslee, Beth

APPLICANT: Larrinua, Ignacio

APPLICANT: Reddy, Avutu

APPLICANT: Shukla, Vipula

APPLICANT: Crosley, Rodney

TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri

FILE REFERENCE: DOW-08552

CURRENT APPLICATION NUMBER: US/10/487,901

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 7560

SOFTWARE: Patentn version 3.1

SEQ ID NO 4354

LENGTH: 593

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic

US-10-487-901-4354

Query Match 97.3%; Score 14.6; DB 21; Length 593;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
|||||:|||||
Db 264 AAGTAAGGCCATTG 250

RESULT 5

US-10-027-632-32790/c
; Sequence 32790, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32790
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-32790

Query Match 97.3%; Score 14.6; DB 13; Length 721;
Best Local Similarity 93.3%; Pred. No. 3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTAAGGCCATTG 15
|||||:|||||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:57:07 ; Search time 31.0185 Seconds
(without alignments)
791.274 Million cell updates/sec

Title: US-10-041-856-86

Perfect score: 15

Sequence: 1 ggttcacagatgtc 15

Scoring table: IDENTITY NUC

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	14.6	97.3	3999	US-09-286-891-1	Sequence 1, Appli
3	13.6	90.7	798	US-09-270-767-13909	Sequence 13909, A
4	13	86.7	242	US-09-270-767-28047	Sequence 28047, A
5	13	86.7	347	US-09-270-767-12302	Sequence 12302, A
6	13	86.7	675	US-09-252-991A-2680	Sequence 2680, Ap
7	13	86.7	1092	US-09-252-991A-2996	Sequence 2996, Ap
8	13	86.7	2544	US-09-252-991A-2775	Sequence 2775, Ap
9	13	86.7	2691	US-09-252-991A-3187	Sequence 3187, Ap
10	13	86.7	3162	US-09-356-643B-12	Sequence 12, Appli
11	13	86.7	3162	US-10-053-510-12	Sequence 12, Appli
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14	13	86.7	818128	US-09-949-016-14547	Sequence 14547, A
15	13	86.7	818128	US-09-949-016-14548	Sequence 14548, A
16	13	86.7	818128	US-09-949-016-14549	Sequence 14549, A
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18	13	86.7	818128	US-09-949-016-14551	Sequence 14551, A
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23	13	86.7	818128	US-09-949-016-14556	Sequence 14556, A
24	13	86.7	818128	US-09-949-016-14557	Sequence 14557, A
25	13	86.7	818128	US-09-949-016-14558	Sequence 14558, A
26	13	86.7	818128	US-09-949-016-14559	Sequence 14559, A
27	13	86.7	818128	US-09-949-016-14560	Sequence 14560, A

28	13	86.7	818128	US-09-949-016-14561	Sequence 14561, A
29	13	86.7	818128	US-09-949-016-14562	Sequence 14562, A
30	13	86.7	818128	US-09-949-016-14563	Sequence 14563, A
31	13	86.7	818128	US-09-949-016-14564	Sequence 14564, A
32	13	86.7	818128	US-09-949-016-14565	Sequence 14565, A
33	13	86.7	818128	US-09-949-016-14566	Sequence 14566, A
34	13	86.7	818128	US-09-949-016-14567	Sequence 14567, A
35	12.6	84.0	756	US-09-949-016-88086	Sequence 88086, A
36	12.6	84.0	756	US-09-270-767-88	Sequence 88, Appli
37	12.6	84.0	756	US-09-270-767-15370	Sequence 15370, A
38	12.6	84.0	837	US-09-134-001C-814	Sequence 814, App
39	12.6	84.0	1434	US-09-540-236-1750	Sequence 1750, App
40	12.6	84.0	1492	US-09-196-520-7	Sequence 7, Appli
41	12.6	84.0	1772	US-09-311-021-139	Sequence 139, App
42	12.6	84.0	1923	US-09-328-352-3932	Sequence 3932, App
43	12.6	84.0	2307	US-09-328-352-276	Sequence 276, App
44	12.6	84.0	3675	US-09-107-532A-2566	Sequence 2566, App
45	12.6	84.0	4224	US-09-328-352-3759	Sequence 3759, App
			8797	US-09-949-016-16186	Sequence 16186, A

ALIGNMENTS

RESULT 1
US-08-971-244-1
Sequence 1, Application US/08971244
Patent No. 5891719
GENERAL INFORMATION:
APPLICANT: Cohen, Lucy
APPLICANT: Bauearle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971.244
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3996
US-08-971-244-1
Query Match 97.3% Score 14.6; DB 2; Length 3999;
Best Local Similarity 93.3%; Pred. No. 34;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 GGTTCACGATGTC 15
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S = G or C

Db 2080 GGTTCACGATTGTC 2094

RESULT 2

US-09-286-891-1
; Sequence 1, Application US/09286891
; Patent No. 6172195
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/286,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/971,244
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
US-09-286-891-1

Query Match 97.3%; Score 14.6; DB 3; Length 3999;

Best Local Similarity 93.3%; Pred. No. 34;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACGATTGTC 15

Db 2080 GGTTCACGATTGTC 2094

RESULT 3

US-09-270-767-13909
; Sequence 13909, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13909
; LENGTH: 798

; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13909

Query Match 90.7%; Score 13.6; DB 4; Length 798;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCACGATTGTC 15

Db 249 GTTCACGATTGTC 262

RESULT 4

US-09-270-767-28047
; Sequence 28047, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 28047
; LENGTH: 242
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28047

Query Match 86.7%; Score 13; DB 4; Length 242;
Best Local Similarity 86.7%; Pred. No. 2.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTTCACGATTGTC 15

Db 143 GTTCACGATTGTC 157

RESULT 5

US-09-270-767-12302
; Sequence 12302, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 12302
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12302

Query Match 86.7%; Score 13; DB 4; Length 347;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTTCACGATTGTC 15

Db 248 GTTCACGATTGTC 262

RESULT 6

US-09-252-991A-2680/c
; Sequence 2680, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:44:02 ; Search time 431.759 Seconds
(without alignments)
1683.411 Million cell updates/sec

Title: US-10-041-856-85

Perfect score: 15

Sequence: 1 aagtaagygccattg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_gy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.6	97.3	15	6	AX676132 Sequence
2	14.6	97.3	312	11	HSPA32D12
3	14.6	97.3	1165	8	AK111717 Oryza sat
4	14.6	97.3	20938	9	AK111717 Oryza sat
5	14.6	97.3	37552	8	AK111717 Oryza sat
6	14.6	97.3	66479	6	AX676132 Sequence
7	14.6	97.3	78376	9	AX676132 Sequence
8	14.6	97.3	83905	2	AL359692 Human DNA
9	14.6	97.3	102200	2	AC025337
10	14.6	97.3	104339	2	AF235105 Human DNA
11	14.6	97.3	105335	8	AF235105 Human DNA
12	14.6	97.3	110000	8	AC107374 Homo sapi
13	14.6	97.3	114581	10	CR182123_10
14	14.6	97.3	146022	10	AL807245 Mouse DNA
15	14.6	97.3	147460	5	AC026881 Homo sapi
16	14.6	97.3	149866	9	AC026881 Homo sapi
17	14.6	97.3	150355	9	AC026881 Homo sapi
18	14.6	97.3	150846	2	AC036173 Homo sapi
19	14.6	97.3	152077	9	HS13062 Human DNA

c	20	14.6	97.3	152448	8	AP004339 Oryza sat
c	21	14.6	97.3	154883	9	AC068711 Homo sapi
c	22	14.6	97.3	158609	2	AC141905 Rattus no
c	23	14.6	97.3	159308	9	AC069277 Homo sapi
c	24	14.6	97.3	162778	9	AC009559 Homo sapi
c	25	14.6	97.3	165049	9	AL159995 Human DNA
c	26	14.6	97.3	166488	9	AC026179 Homo sapi
c	27	14.6	97.3	167726	2	AC012580 Homo sapi
c	28	14.6	97.3	167726	2	AC115898 Mus muscu
c	29	14.6	97.3	173292	2	CNS01DVA Human chr
c	30	14.6	97.3	174208	2	AC015935 Homo sapi
c	31	14.6	97.3	175780	2	AC138678 Mus muscu
c	32	14.6	97.3	185196	2	AC023939 Mus muscu
c	33	14.6	97.3	191304	5	AL928675 Zebrafish
c	34	14.6	97.3	194201	2	AC148038 Ovis arie
c	35	14.6	97.3	204794	2	AC024897 Homo sapi
c	36	14.6	97.3	204797	9	AC024154 Homo sapi
c	37	14.6	97.3	213701	10	AC125410 Mus muscu
c	38	14.6	97.3	217043	2	AC026932 Homo sapi
c	39	14.6	97.3	217912	2	AC094349 Rattus no
c	40	14.6	97.3	223854	10	AL606962 Mouse DNA
c	41	14.6	97.3	224391	2	AC148953 Oryza sat
c	42	14.6	97.3	235033	6	BD084121 Polymorph
c	43	14.6	97.3	236644	2	AC109122 Rattus no
c	44	14.6	97.3	237326	6	BD084122 Polymorph
c	45	14.6	97.3	246240	6	AR036572 Sequence

ALIGNMENTS

RESULT 1

AX676132

LOCUS AX676132 Sequence 85 from Patent WO02059381. 15 bp DNA

DEFINITION AX676132

ACCESSION AX676132

VERSION AX676132.1 GI:29333816

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1

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1

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 09:42:59 ; Search time 106.204 Seconds
(without alignments)
836.092 Million cell updates/sec

Title: US-10-041-856-85

Perfect score: 15

Sequence: 1 aagtaagycgcatcg 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

8780412

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.6	97.3	15	6	ABQ80561
2	14.6	97.3	369	10	ADK56433
3	14.6	97.3	593	10	ADK56971
4	14.6	97.3	66479	6	ABQ80567
5	14.6	97.3	66479	6	ABQ80566
6	14.6	97.3	66479	6	ABQ80568
7	14.6	97.3	66479	6	ABQ80565
8	14.6	97.3	237326	2	AAV57903
9	13.6	90.7	328	6	ABQ67963
10	13.6	90.7	390	10	ADH83551
11	13.6	90.7	430	6	ABK30463
12	13.6	90.7	570	6	AAK96719
13	13.6	90.7	570	11	ADM39599
14	13.6	90.7	595	6	AAK96714
15	13.6	90.7	595	11	ADM39589
16	13.6	90.7	751	10	ADK60125
17	13.6	90.7	1020	2	AAT40142
18	13.6	90.7	1446	6	ABZ78269
19	13.6	90.7	1453	2	AAK13183
20	13.6	90.7	1453	6	ABK98978

C	21	13.6	90.7	1587	13	ADR88965	Adr88965 A. thalia
C	22	13.6	90.7	1957	4	ABA46165	ABA46165 Human bre
C	23	13.6	90.7	1957	4	AAK30368	AAK30368 Human bon
C	24	13.6	90.7	2360	2	AAT40148	Aat40148 A. niger
C	25	13.6	90.7	2520	6	ABZ78212	Abz78212 A. niger
C	26	13.6	90.7	3105	10	ADF03715	Adf03715 Bacterial
C	27	13.6	90.7	3172	13	ADS10043	Ads10043 Human the
C	28	13.6	90.7	3774	4	AAK70878	AAK70878 Human imm
C	29	13.6	90.7	6242	6	ABQ70961	Abq70961 Listeria
C	30	13.6	90.7	7355	12	ADN49781	Adn49781 Turkey as
C	31	13.6	90.7	12462	4	ABL05490	Ab105490 Drosophila
C	32	13.6	90.7	12481	4	ABL20544	Ab120544 Drosophila
C	33	13.6	90.7	13417	2	AAT09224	Aat09224 Partial s
C	34	13.6	90.7	26705	12	ADQ62810	Adq62810 Pseudomon
C	35	13.6	90.7	32986	4	AAK69758	Aak69758 Human imm
C	36	13.6	90.7	32986	4	AAK84629	Aak84629 Human imm
C	37	13.6	90.7	50000	2	AAK23517	Aak23517 Human kid
C	38	13.6	90.7	56258	11	ACN44456	Acn44456 Mouse gen
C	39	13.6	90.7	62488	6	AAD44981	Aad44981 Human EMR
C	40	13.6	90.7	110000	6	ABQ69245_14	Continuation (15 o
C	41	13.6	90.7	110000	6	ABQ67195_3	Continuation (4 of
C	42	13.6	90.7	110000	6	ABA03041_14	Continuation (15 o
C	43	13.6	90.7	151152	13	ADR52892	Adr52892 Drug ther
C	44	13.6	90.7	163382	13	ABD32659	Abd32659 Human can
C	45	13.6	90.7	349980	6	ABQ81845	Abq81845 Bifidobac

ALIGNMENTS

RESULT 1	ABQ80561	ABQ80561 standard; DNA, 15 BP.
ID	ABQ80561	
XX	ABQ80561	
AC	ABQ80561	
DT	08-NOV-2002	(first entry)
XX		
DE	IKKAP probe #1.	
XX		
KW	Human; IKKAP; Familial Dysautonomia; FD; Riley-Day syndrome;	
KW	Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;	
KW	probe; ss.	
OS	Homo sapiens.	
PN	W0200259381-A2.	
PD		
XX	01-AUG-2002.	
PE		
XX	07-JAN-2002; 2002W0-US000473.	
XX		
PR	06-JAN-2001; 2001US-026080P.	
PA	(GEHO) GEN HOSPITAL CORP.	
XX		
PI	Slangenhaup S, Gueella JF;	
DR	WPI; 2002-674806/72.	
XX		
PT	New IKKAP genes with mutations, useful for identifying a subject with	
PT	familial dysautonomia (FD), or for rapid carrier screening in the	
PT	Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or	
PT	prenatal diagnosis.	
PS	Claim 27; Page 43; 109pp; English.	
XX		
CC	The present invention relates to methods and compositions useful for	
CC	detecting mutations which cause Familial Dysautonomia (FD, Riley-Day	
CC	syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM	
CC	223900). It was found that mutations in the IKKAP gene (see ABQ80565)	
CC	are associated with FD. The mutation associated with the major haplotype	
CC	of FD, FDI mutation, is a base pair (bp) mutation, where the thymine	

CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from PD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, PD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2297 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKKAP nucleic acid sequences are useful for
CC identifying a subject with PD and for rapid carrier screening. The IKKAP
CC gene maps to chromosome 9q31. Probes ABQ80561-ABQ80562 were used to
CC detect the mutations in the IKKAP gene
XX
SQ Sequence 15 BP; 5 A; 2 C; 4 G; 3 T; 0 U; 1 Other;
Query Match 97.3%; Score 14.6; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGTAAGGCCATTG 15
Db 1 AAGTAAGGCCATTG 15
RESULT 2
ADK56433/c
ID ADK56433 standard; DNA; 369 BP.
XX
AC ADK56433;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant DNA sequence which confers altered metabolic characteristic #3816.
XX
KM altered metabolic characteristic; plant; acid metabolism;
KM alcohol metabolism; fatty acid metabolism;
KM branched fatty acid metabolism; alkaloid metabolism;
KM amino acid metabolism; ester metabolism; glyceride metabolism;
KM phenolic metabolism; carbohydrate metabolism; steroid metabolism;
KM terpene metabolism; isoprenoid metabolism; alkene metabolism;
KM alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KM quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS Hypocrea lixii.
XX
PN WO2003020936-A1.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002MO-US027884.
XX
PR 31-AUG-2001; 2001US-0316471P.
XX
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGRSCIENCES LLC.
XX
PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX
DR WPI; 2003-313091/30.
XX
PT Novel genes that confer altered metabolic characteristics in Nicotiana
PT benthamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
PS Claim 1; SEQ ID NO 3816; 2576bp; English.
XX
CC The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC isoprenoid metabolism, altered steroid, oxygenated terpene, or
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene

CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered steroid, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.
XX
SQ Sequence 369 BP; 125 A; 70 C; 75 G; 99 T; 0 U; 0 Other;
Query Match 97.3%; Score 14.6; DB 10; Length 369;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGTAAGGCCATTG 15
Db 43 AAGTAAGGCCATTG 29
RESULT 3
ADK56971/c
ID ADK56971 standard; DNA; 593 BP.
XX
AC ADK56971;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant DNA sequence which confers altered metabolic characteristic #4354.
XX
KM altered metabolic characteristic; plant; acid metabolism;
KM alcohol metabolism; fatty acid metabolism;
KM branched fatty acid metabolism; alkaloid metabolism;
KM amino acid metabolism; ester metabolism; glyceride metabolism;
KM phenolic metabolism; carbohydrate metabolism; steroid metabolism;
KM terpene metabolism; isoprenoid metabolism; alkene metabolism;
KM alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KM quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS Unidentified.
XX
PN WO2003020936-A1.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002MO-US027884.
XX
PR 31-AUG-2001; 2001US-0316471P.
XX
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGRSCIENCES LLC.
XX
PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX
DR WPI; 2003-313091/30.
XX
PT Novel genes that confer altered metabolic characteristics in Nicotiana
PT benthamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
PS Claim 1; SEQ ID NO 4354; 2576bp; English.
XX
CC The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered steroid, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene

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OM nucleic - nucleic search, using sw model

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Title: US-10-041-856-86

Perfect score: 15

Sequence: 1 ggtcaccgattctc 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.6	97.3	15	ABQ80562	Abq80562 IKBKAP pr
2	14.6	97.3	803	AAH05318	Aah05318 Human CDN
3	14.6	97.3	2471	AAH15795	Aah15795 Human CDN
4	14.6	97.3	3999	AAH28025	Aah28025 Human IKA
5	14.6	97.3	3999	AAH29756	Aah29756 Human IKA
6	14.6	97.3	4417	AAH07102	Aah07102 Full leng
7	14.6	97.3	4788	AAH14533	Aah14533 Human CDN
8	14.6	97.3	4803	AAH14533	Aah14533 Human dif
9	14.6	97.3	4803	AAH14533	Aah14533 Human dif
10	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
11	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
12	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
13	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
14	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
15	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
16	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
17	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
18	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
19	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu
20	14.6	97.3	5924	ABQ80562	Abq80562 Mutant hu

c 21	13.6	90.7	110000	10	ACF65383.1	Continuation (2 of
c 22	13.6	90.7	110000	10	ACF67367.02	Continuation (3 of
c 23	13.6	90.7	110000	10	ACF67367.25	Continuation (26 of
c 24	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 25	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 26	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 27	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 28	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 29	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 30	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 31	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 32	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 33	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 34	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 35	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 36	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 37	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 38	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 39	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 40	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 41	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 42	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 43	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 44	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of
c 45	13.6	90.7	110000	10	ACF65386_3	Continuation (4 of

ALIGNMENTS

RESULT 1	ABQ80562	standard; DNA; 15 BP.
ID	ABQ80562	standard; DNA; 15 BP.
AC	ABQ80562	
DT	08-NOV-2002	(first entry)
XX	IKBKAP probe #2.	
XX	Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;	
XX	Hereditary Sensory and Autonomic Neuropathy Type II; carrier screening;	
XX	probe; ss.	
XX	Homo sapiens.	
XX	W0200259381-A2.	
XX	01-AUG-2002.	
XX	07-JAN-2002; 2002WO-US000473.	
XX	06-JAN-2001; 2001US-0260080P.	
XX	(GENO) GEN HOSPITAL CORP.	
XX	Slangenheut S, Gusella JF;	
XX	WPI; 2002-674806/72.	
XX	New IKBKAP gene with mutations, useful for identifying a subject with	
XX	familial dysautonomia (FD), or for rapid carrier screening in the	
XX	Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or	
XX	prenatal diagnosis.	
XX	Claim 27; Page 43; 109pp; English.	
XX	The present invention relates to methods and compositions useful for	
XX	detecting mutations which cause Familial Dysautonomia (FD, Riley-Day	
XX	syndrome, Hereditary Sensory and Autonomic Neuropathy Type II) (OMIM	
XX	223900). It was found that mutations in the IKBKAP gene (see ABQ80562)	
XX	are associated with FD. The mutation associated with the major haplotype	
XX	of FD, FDI mutation, is a base pair (bp) mutation, where the thymine	

CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from PD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, PD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2297 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKKAP nucleic acid sequences are useful for
CC identifying a subject with PD and for rapid carrier screening. The IKKAP
CC gene maps to chromosome 9q31. Probes AB080561-AB080562 were used to
CC detect the mutations in the IKKAP gene

XX
SQ Sequence 15 BP; 2 A; 3 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 97.3%; Score 14.6; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCACSGATTGTC 15
Db 1 GGTTCACSGATTGTC 15

RESULT 2
AAH05318
ID AAH05318 standard; cDNA; 803 BP.
XX
XX AAH05318;
AC
XX 26-JUN-2001 (first entry)
DT
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:2153.
XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
PD
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-00116126.
PF
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
XX Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PI
XX WPI; 2001-318749/34.
DR
XX
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

XX
PS Claim 1; SEQ ID NO 2153; 2537bp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH11633 to AAH18742 represent human cDNA sequences; AAH93446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX
SQ Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;

Query Match 97.3%; Score 14.6; DB 4; Length 803;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCACSGATTGTC 15
Db 72 GGTTCACSGATTGTC 86

RESULT 3
AAH15795
ID AAH15795 standard; cDNA; 2471 BP.
XX
XX AAH15795;
AC
XX 26-JUN-2001 (first entry)
DT
XX
DE Human cDNA sequence SEQ ID NO:14253.
XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
PD
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-00116126.
PF
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
XX Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PI
XX WPI; 2001-318749/34.
DR
XX
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

XX
PS Claim 8; SEQ ID NO 14253; 2537bp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 16:38:33 ; Search time 153.148 Seconds
(without alignments)
633.931 Million cell updates/sec

Title: US-10-041-856-86
Perfect score: 15
Sequence: 1 ggtccacgattgtc 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.6	97.3	15	US-10-041-856-86	Sequence 86, Appl
2	14.6	97.3	201	US-10-719-993-4499	Sequence 4499, Ap
3	14.6	97.3	201	US-10-719-993-4527	Sequence 4527, Ap
4	14.6	97.3	201	US-10-719-993-4556	Sequence 4556, Ap
5	14.6	97.3	201	US-10-719-993-4585	Sequence 4585, Ap
6	14.6	97.3	201	US-10-719-993-4613	Sequence 4613, Ap
7	14.6	97.3	201	US-10-719-993-34995	Sequence 34995, A

8	14.6	97.3	4256	20	US-10-719-993-319	Sequence 319, App
9	14.6	97.3	4803	21	US-09-930-213-276	Sequence 276, App
10	14.6	97.3	4803	20	US-10-956-157-1094	Sequence 1094, Ap
11	14.6	97.3	5840	20	US-10-719-993-322	Sequence 322, App
12	14.6	97.3	5924	13	US-10-041-856-2	Sequence 2, Appl1
13	14.6	97.3	5957	20	US-10-719-993-320	Sequence 320, App
14	14.6	97.3	6107	20	US-10-719-993-321	Sequence 321, App
15	14.6	97.3	6179	20	US-10-719-993-318	Sequence 318, App
16	14.6	97.3	6479	13	US-10-041-856-1	Sequence 1, Appl1
17	14.6	97.3	78878	20	US-10-719-993-6863	Sequence 6863, Ap
18	13.4	89.3	25	21	US-10-719-900-622520	Sequence 622520,
19	13.4	89.3	2365	18	US-10-424-599-141749	Sequence 141749,
20	13	86.7	25	21	US-10-719-900-2420	Sequence 2420, Ap
21	13	86.7	25	21	US-10-719-900-718633	Sequence 718633,
22	13	86.7	25	22	US-10-719-956-459049	Sequence 459049,
23	13	86.7	25	22	US-10-719-956-534331	Sequence 534331,
24	13	86.7	253	18	US-10-424-599-67860	Sequence 67860, A
25	13	86.7	330	18	US-10-389-647-44	Sequence 44, Appl
26	13	86.7	369	9	US-09-983-965-694	Sequence 894, App
27	13	86.7	386	20	US-10-425-115-102611	Sequence 102611,
28	13	86.7	402	17	US-10-398-221-304	Sequence 304, App
29	13	86.7	408	13	US-10-027-632-44467	Sequence 44467, A
30	13	86.7	408	17	US-10-027-632-44467	Sequence 44467, A
31	13	86.7	409	13	US-10-027-632-66788	Sequence 66788, A
32	13	86.7	409	13	US-10-027-632-67332	Sequence 67332, A
33	13	86.7	409	13	US-10-027-632-311246	Sequence 311246,
34	13	86.7	409	13	US-10-027-632-311247	Sequence 311247,
35	13	86.7	409	17	US-10-027-632-66788	Sequence 66788, A
36	13	86.7	409	17	US-10-027-632-311246	Sequence 311246,
37	13	86.7	409	17	US-10-027-632-311247	Sequence 311247,
38	13	86.7	414	20	US-10-425-115-123345	Sequence 123345,
39	13	86.7	409	17	US-10-425-115-173809	Sequence 173809,
40	13	86.7	524	20	US-10-425-115-35913	Sequence 35913, A
41	13	86.7	533	18	US-10-282-1224-8377	Sequence 8377, App
42	13	86.7	546	9	US-09-974-300-3577	Sequence 3577, App
43	13	86.7	564	9	US-09-770-152-372	Sequence 372, App
44	13	86.7	546	9	US-10-027-632-245629	Sequence 245629,
45	13	86.7	624	13		

ALIGNMENTS

RESULT 1
US-10-041-856-86
; Sequence 86, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041, 856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-041-856-86

Query Match 97.3%; Score 14.6; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTCCACGATTGTC 15
|||||

Db 1 GGTTCACSGATTGTC 15

RESULT 2

US-10-719-993-4499
; Sequence 4499, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4499
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4499

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACSGATTGTC 15
|||
Db 94 GGTTCACSGATTGTC 108

RESULT 3

US-10-719-993-4527
; Sequence 4527, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4527
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4527

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACSGATTGTC 15
|||
Db 94 GGTTCACSGATTGTC 108

RESULT 4

US-10-719-993-4556
; Sequence 4556, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4556

; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4556

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACSGATTGTC 15
|||
Db 94 GGTTCACSGATTGTC 108

RESULT 5

US-10-719-993-4585
; Sequence 4585, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4585
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4585

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACSGATTGTC 15
|||
Db 94 GGTTCACSGATTGTC 108

RESULT 6

US-10-719-993-4613
; Sequence 4613, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4613
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4613

Query Match 97.3%; Score 14.6; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACSGATTGTC 15
|||
Db 94 GGTTCACSGATTGTC 108

RESULT 7

US-10-719-993-34995
; Sequence 34995, Application US/10719993

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 734.537 Seconds
(without alignments)
777.311 Million cell updates/sec

Title: US-10-041-856-86

Perfect score: 15

Sequence: 1 ggttcacgattgtc 15

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.6	97.3	417	7	CN256146 170005321
2	14.6	97.3	447	2	BF840993 RC3-HT097
3	14.6	97.3	513	1	AL702133 DKF2P686G
4	14.6	97.3	524	4	BI647985 603276059
5	14.6	97.3	553	4	BM512007 1177d11.x
6	14.6	97.3	567	7	CO794653 NT144A.H1
7	14.6	97.3	580	5	BP243833 BP243833
8	14.6	97.3	603	5	BK478139 DKF2P686B
9	14.6	97.3	618	4	BG395601 602458222
10	14.6	97.3	641	5	BQ807986 NISC.K12
11	14.6	97.3	686	8	BH985208 oe169d05
12	14.6	97.3	694	5	BP152797 BP152797
13	14.6	97.3	709	7	CN256149 170004241
14	14.6	97.3	777	8	BH944352 cbu89b12
15	14.6	97.3	803	1	AU124100 AU124100
16	14.6	97.3	866	5	BU508979 AGENCOURT
17	14.6	97.3	874	5	BU156074 AGENCOURT
18	14.6	97.3	911	4	BE256729 601115546
19	14.6	97.3	931	4	BG286503 602382995
20	14.6	97.3	982	8	BZ786955 PUGB42TB
21	14.6	97.3	1134	7	CN641371 ILUDWIGEN
22	14.6	97.3	1833	3	CR749385 Homo sapi
23	14.6	97.3	3999	9	AY414501 Homo sapi
24	14.6	97.3	3999	9	AY414502 Pan trogl

25	13.6	90.7	247	1	AA260845
26	13.6	90.7	258	6	CA609548
27	13.6	90.7	260	8	AQ073317
28	13.6	90.7	269	1	A1896149
29	13.6	90.7	295	9	CC848090
30	13.6	90.7	300	7	CO278011
31	13.6	90.7	311	2	AM031051
32	13.6	90.7	321	6	CA639543
33	13.6	90.7	322	6	CA649351
34	13.6	90.7	338	6	CA652678
35	13.6	90.7	340	6	CA612274
36	13.6	90.7	368	3	CNS08VRT
37	13.6	90.7	373	4	BG141075
38	13.6	90.7	381	2	AW217022
39	13.6	90.7	401	4	BI422386
40	13.6	90.7	401	6	BI601592
41	13.6	90.7	427	8	BH818839
42	13.6	90.7	436	6	CA640314
43	13.6	90.7	445	1	A1895520
44	13.6	90.7	449	1	A1293974
45	13.6	90.7	458	2	AW344428

ALIGNMENTS

RESULT 1
CN256146 17000532188935 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN256146 1 GI:47272560

LOCUS CN256146 417 bp mRNA linear EST 16-MAY-2004

DEFINITION CN256146

ACCESSION CN256146

VERSION CN256146.1 GI:47272560

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 417)

AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R

Genetivative Medicine

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genetiv.com

Insert Length: 417 Std Error: 0.00.

Location/Qualifiers

1..417

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"

/clone_lib="GRN ES"

/note="Oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p23), H7 (p23), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

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Best Local Similarity 93.3% Pred. No. 5e+02;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCACGATTGTC 15

DB 184 GGTTCACGATTGTC 198

RESULT 2
BF840993/c 447 bp mRNA linear EST 13-JAN-2001
LOCUS
DEFINITION RC3-HT0974-011200-013-a03 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF840993
VERSION BF840993.1 GI:12193641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 20202663
COMMENT 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&ct=RC3-HT0974-
011200-013-a03&cs=2000-12-01&ct=1)
Seq primer: puc 18 forward
High quality sequence start: 29
High quality sequence stop: 447.
Location/Qualifiers
1..447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="HT0974"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 97.3%; Score 14.6; DB 2; Length 447;
Best Local Similarity 93.3%; Pred. No. 5.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCACSGATTGTC 15
|||||:|||||
Db 319 GGTTACAGGATTGTC 305

RESULT 3
AL702133 513 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION DKFZp686G02155.t1.686 (synonym: h1cc3) Homo sapiens cDNA clone
ACCESSION DKFZp686G02155.5, mRNA sequence.
VERSION AL702133
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 513)
AUTHORS Bloeker,H., Boecker,M., Brandt,P., Mewes,W., Weil,B. and
Wiemann,S.
TITLE EST (Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B. and
Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by GFP (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZp686G02155) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..513
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G02155"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: h1cc3)"
/note="Vector: pTrioPlx2; Site 1: SfiI; Site 2: SfiI;
cDNA-collection"

ORIGIN
Query Match 97.3%; Score 14.6; DB 1; Length 513;
Best Local Similarity 93.3%; Pred. No. 5.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCACSGATTGTC 15
|||||:|||||
Db 292 GGTTACAGGATTGTC 306

RESULT 4
BI647985/c 524 bp mRNA linear EST 12-SEP-2001
LOCUS
DEFINITION 603276059F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5316470 5',
mRNA sequence.
ACCESSION BI647985
VERSION BI647985.1 GI:15562208
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 524)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cga@bs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM1802 row e column: 15
High quality sequence start: 196
High quality sequence stop: 522.
Location/Qualifiers

FEATURES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:44:02 ; Search time 546.895 Seconds
(without alignments)
1683.411 Million cell updates/sec

Title: US-10-041-856-82

Perfect score: 19
Sequence: 1 gccagtgcttgcctgag 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sls:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	AX676129 Sequence
2	19	100.0	3516	6	CQ724004 Sequence
3	19	100.0	3999	6	AR070165 Sequence
4	19	100.0	3999	6	AR124807 Sequence
5	19	100.0	4417	6	CQ850139 Sequence
6	19	100.0	4417	9	AK127237 Homo sapi
7	19	100.0	4788	6	BD156525 Primer fo
8	19	100.0	4788	6	AX877177 Sequence
9	19	100.0	4788	6	AK001641 Homo sapi
10	19	100.0	4803	6	BD171366 Method fo
11	19	100.0	4803	6	BD173600 Method of
12	19	100.0	4803	6	AX10634 Sequence
13	19	100.0	4803	6	AF044195 Homo sapi
14	19	100.0	5047	9	BC033094 Homo sapi
15	19	100.0	5924	6	AX676049 Sequence
16	19	100.0	5924	6	AF153419 Homo sapi
17	19	100.0	66479	6	AX676048 Sequence
18	19	100.0	78376	9	AL159692 Human DNA
19	19	94.7	392	6	AX210429 Sequence

C	20	18	94.7	181675	2	AC113990
	21	17.4	91.6	722295	2	AC027050
	22	17.4	91.6	109156	9	AB065679
	23	17.4	91.6	117636	9	HSJ365012
	24	17.4	91.6	158391	10	AC115051
	25	17.4	91.6	164603	2	AC119466
	26	17.4	91.6	180338	10	AC090496
	27	17.4	91.6	183146	9	AC116697
	28	17.4	91.6	186113	9	AC123097
	29	17.4	91.6	219340	10	AL844881
	30	17.4	91.6	219714	2	AC096601
	31	17.4	91.6	223966	2	AC094504
	32	17.4	91.6	235660	2	AC128377
	33	17.4	91.6	267540	2	AC107153
	34	17.4	89.5	1525	5	KL093302
	35	17	89.5	110000	1	EX950851_49
	36	17	89.5	126118	9	AC104598
	37	17	89.5	150641	9	AC092153
	38	17	89.5	151046	10	AC111104
	39	17	89.5	189666	10	AC102155
	40	17	89.5	197025	2	AC118442
	41	17	89.5	201478	10	AC132608
	42	17	89.5	234795	10	AC099934
	43	17	89.5	235978	2	AC116249
	44	17	89.5	243910	2	AC096208
	45	17	89.5	317634	2	AC150936

ALIGNMENTS

RESULT 1
AX676129
LOCUS AX676129 Sequence 82 from Patent WO02059381.
DEFINITION AX676129
ACCESSION AX676129
VERSION AX676129.1 GI:29333813
KEYWORDS
ORGANISM
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Slangenhuysen, S. and Guesella, J.F.
TITLRE Gene for identifying individuals with familial dysautonomia
JOURNAL Patent: WO 02059381-A 82 01-AUG-2002;
The General Hospital Corporation (US)
FEATURES
source
1..19
location/Qualifiers
/organism="synthetic construct"
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/note="Primer"

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCAGTGTTCCTGAG 19
DB 1 GCCAGTGTTCCTGAG 19
RESULT 2
LOCUS CQ724004 3516 bp DNA
DEFINITION Sequence 9938 from Patent WO0206579.
ACCESSION CQ724004
VERSION CQ724004.1 GI:42284861
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE KIts, such as nucleic acid arrays, comprising a majority of humamexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 9938 06-SEP-2002;
PE Corporation (NY) (US)

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTGTTTGCTGAG 19
Db 1763 GCCAGTGTGTTTGCTGAG 1761

RESULT 3
LOCUS AR070165 3999 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5891719.
ACCESSION AR070165
VERSION AR070165.1 GI:7221053

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3999)
AUTHORS Cohen,L. and Baeruerle,P.
TITLE IKAP nucleic acids

JOURNAL Patent: US 5891719-A 1 06-APR-1999;
FEATURES Location/Qualifiers
source 1. .3999
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Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTGTTTGCTGAG 19
Db 1979 GCCAGTGTGTTTGCTGAG 1997

RESULT 4
LOCUS AR124807 3999 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6172195.
ACCESSION AR124807
VERSION AR124807.1 GI:14110168

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3999)
AUTHORS Cohen,L. and Baeruerle,P.
TITLE IKAP proteins and methods

JOURNAL Patent: US 6172195-A 1 09-JAN-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTGTTTGCTGAG 19
Db 1979 GCCAGTGTGTTTGCTGAG 1997

RESULT 5
LOCUS CO850139 4417 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 608 from Patent EP1447413.
ACCESSION CO850139
VERSION CO850139.1 GI:51508351

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Isegai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
TITLE Full-length human cDNA
JOURNAL Patent: EP 1447413-A 608 18-AUG-2004;
FEATURES Research Association for Biotechnology (JP)

source 1. .4417
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Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1918 GCCAGTGTGTTTGCTGAG 1936

RESULT 6
LOCUS AK127237 4417 bp mRNA linear PRI 19-FEB-2004
DEFINITION Homo sapiens cDNA FLJ45304 fls, clone BRH1P3003984, highly similar to Ikappab kinase complex-associated protein.

ACCESSION AK127237
VERSION AK127237.1 GI:34534066
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Ohnita,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
Arita,M., Msaashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Magaesuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
Suzuki,Y., Sugano,S., Nagahara,K., Maseho,Y., Nagai,K. and
Isegai,T.

NEO human cDNA sequencing project
Unpublished

REFERENCE 2 (bases 1 to 4417)
AUTHORS Isegai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2003) Takao Isegai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genome@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3966)

NEO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 09:42:59 ; Search time 134.525 Seconds
(without alignments)
836.092 Million cell updates/sec

Title: US-10-041-856-82

Perfect score: 19
Sequence: 1 gccacgtcttcgtcgtcag 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	ABQ80558	IKBKAP PC
2	19	100.0	3999	AAx28025	Human IKA
3	19	100.0	3999	AAx29756	Human IKA
4	19	100.0	4417	ADRO7102	Full leng
5	19	100.0	4788	AAH14533	Human CDN
6	19	100.0	4803	AAH81767	Human dif
7	19	100.0	4803	AAH44190	Human I-k
8	19	100.0	5924	ABQ80570	Mutant hu
9	19	100.0	5924	ABQ80569	Human IKB
10	19	100.0	5924	ABQ80568	Human IKB
11	19	100.0	66479	ABQ80567	Mutant hu
12	19	100.0	66479	ABQ80566	Mutant hu
13	19	100.0	66479	ABQ80565	Mutant hu
14	19	100.0	66479	ABQ80564	Mutant hu
15	18	94.7	392	AAH81562	Human dif
16	16.4	86.3	482	ADQ21369	Human sof
17	16.4	86.3	5550	AB108413	Drosophi1
18	16.4	86.3	7887	AB108412	Drosophi1
19	16.4	86.3	14117	AB277045	Bovine DG
20	16.4	86.3	14117	AB277044	Bovine DG

21	16	84.2	432	8	ABX43560
22	16	84.2	770	2	AAV28664
23	16	84.2	180550	10	ADL13850
24	15.8	83.2	20	2	AAZ03131
25	15.8	83.2	171	8	ABZ19361
26	15.8	83.2	202	4	AAI24501
27	15.8	83.2	203	11	ADT97815
28	15.8	83.2	259	4	AAI15657
29	15.8	83.2	1011	2	AAZ27728
30	15.8	83.2	1011	2	AAZ27729
31	15.8	83.2	1271	11	ACN85637
32	15.8	83.2	1519	6	ABK34935
33	15.8	83.2	1665	3	AAK47898
34	15.8	83.2	2488	10	ADB62749
35	15.8	83.2	2495	8	ABT32174
36	15.8	83.2	2547	4	AAH13749
37	15.8	83.2	2666	13	ABD33352
38	15.8	83.2	3788	4	AAK33107
39	15.8	83.2	4463	2	AAV62085
40	15.8	83.2	4463	2	AAV62084
41	15.8	83.2	6057	8	ABX63239
42	15.8	83.2	6111	13	ACN40249
43	15.8	83.2	6330	5	ABV30125
44	15.8	83.2	6342	11	ACN92292
45	15.8	83.2	9528	4	ABL19946

ALIGNMENTS

RESULT 1
ABQ80558
ID ABQ80558 standard; DNA, 19 BP.
XX
XX ABQ80558;
XX
DT 08-NOV-2002 (first entry)
XX
DE IKBKAP PCR primer 18F.
XX
KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200259381-A2.
XX
PD 01-AUG-2002.
XX
PF 07-JAN-2002; 2002WO-US000473.
XX
PR 06-JAN-2001; 2001US-026080P.
PA (GEO) GEN HOSPITAL CORP.
PI Slangenaupt S, Guesella JF;
PI WPI; 2002-674806/72.
DR
PT New IKBKAP genes with mutations, useful for identifying a subject with
PT familial dysautonomia (FD), or for rapid carrier screening in the
PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT prenatal diagnosis.
PS
PX Claim 33; Page 27; 109pp; English.
XX
CC The present invention relates to methods and compositions useful for
CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM
CC 223900). It was found that mutations in the IKBKAP gene (see ABQ80565)
CC are associated with FD. The mutation associated with the major haplotype
CC of FD, FDI mutation, is a base pair (bp) mutation, where the thymine

CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from PD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, PD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKKAP nucleic acid sequences are useful for
CC identifying a subject with PD and for rapid carrier screening. The IKKAP
CC gene maps to chromosome 9q31. PCR primers ABQ80558-ABQ80560 were used to
CC detect the splicing defect in IKKAP gene
XX
SQ Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGTGTGCTGAG 19
Db 1 GCCAGTGTGCTGAG 19
XX
RESULT 2
AAK28025
ID AAK28025 standard; cDNA; 3999 BP.
XX
AC AAK28025;
XX
DT 09-JUN-1999 (first entry)
XX
DE Human IKAP coding sequence.
XX
KW IKAP: human; cellular signal transduction regulator;
KM transcriptional activation regulator; translatable transcript; ds.
XX
OS Homo sapiens.
XX
PN US5891719-A.
XX
PD 06-APR-1999.
XX
PF 16-NOV-1997; 97US-00971244.
XX
PR 16-NOV-1997; 97US-00971244.
XX
PS (TUL-) TULARIK INC.
XX
PI Cohen L, Baeuerle P;
XX
DR WPI; 1999-253865/21.
DR P-PSDB; AAY01084.
XX
PT Isolated, recombinant cDNA sequences encoding human IKAP polypeptides -
PT useful for regulating cellular signal transduction and transcriptional
PT activation.
XX
PS Claim 23; Col 9-18; 15pp; English.
XX
CC This sequence encodes the human IKAP protein of the invention. IKAP
CC regulates cellular signal transduction and transcriptional activation
CC (e.g. the activation of nuclear factor kappaB). Nucleic acids encoding
CC IKAP have a range of applications including use as translatable
CC transcripts, hybridisation probes, polymerase chain reaction (PCR)
CC primers, diagnostic nucleic acids, use in detecting the presence of IKAP
CC genes and gene transcripts and in detecting or amplifying nucleic acids
CC encoding additional IKAP homologues and structural analogues. In
CC diagnosis IKAP hybridisation probes may be used to identify wild-type and
CC mutant IKAP alleles in clinical samples. In therapy, IKAP nucleic acids
CC can be used to modulate cellular expression or intracellular
CC concentration or availability of active IKAP
XX

SQ Sequence 3999 BP; 1110 A; 851 C; 995 G; 1043 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGTGTGCTGAG 19
Db 1979 GCCAGTGTGCTGAG 1997
XX
RESULT 3
AAF29756
ID AAF29756 standard; cDNA; 3999 BP.
XX
AC AAF29756;
XX
DT 05-APR-2001 (first entry)
XX
DE Human IKAP coding sequence.
XX
KW Human; IKAP: signal transduction; NIK binding activity;
KM transcription factor; diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
PN US6172195-B1.
XX
PD 09-JAN-2001.
XX
PF 06-APR-1999; 99US-00286891.
XX
PR 16-NOV-1997; 97US-00971244.
XX
PS (TUL-) TULARIK INC.
XX
PI Cohen L, Baeuerle P;
XX
DR WPI; 2001-158378/16.
DR P-PSDB; AAB66345.
XX
PT Novel human kinase IKAP polypeptide useful in diagnosis, therapy,
PT biopharmaceutical industry and for screening for modulators of the
PT polypeptide.
XX
PS Disclosure; Col 9-18; 15pp; English.
XX
CC The present invention provides the human IKAP protein. This is involved
CC in signal transduction pathways, where it binds to NIK and results in the
CC activation of transcription factors. The protein and its coding sequence
CC can be used in disease diagnosis and therapy, as well as in the
CC biopharmaceutical industry
XX
SQ Sequence 3999 BP; 1110 A; 851 C; 995 G; 1043 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 4; Length 3999;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGTGTGCTGAG 19
Db 1979 GCCAGTGTGCTGAG 1997
XX
RESULT 4
ADR07102
ID ADR07102 standard; cDNA; 4417 BP.
XX
AC ADR07102;
XX
DT 04-NOV-2004 (first entry)
XX
DE Full length human cDNA useful for treating neurological disease Seq 608.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:57:07 ; Search time 39.2901 Seconds
(without alignments)
791.274 Million cell updates/sec

Title: US-10-041-856-82

Perfect score: 19

Sequence: 1 gccagtgcttgcctgag 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTCUTS.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	3999	2	US-08-971-244-1
2	19	100.0	3999	3	US-09-286-891-1
3	15.8	83.2	601	4	US-09-949-016-68848
4	15.8	83.2	601	4	US-09-949-016-68849
5	15.8	83.2	1011	3	US-09-018-584A-28
6	15.8	83.2	1011	3	US-09-018-584A-29
7	15.8	83.2	1011	4	US-09-784-423-28
8	15.8	83.2	1011	4	US-09-784-423-29
9	15.8	83.2	4463	2	US-08-760-489-1
10	15.8	83.2	4463	2	US-08-760-489-3
11	15.8	83.2	4463	3	US-09-185-373-1
12	15.8	83.2	4463	3	US-09-185-373-3
13	15.8	83.2	4463	4	US-09-949-016-13765
14	15.4	81.1	601	4	US-09-949-016-29141
15	15.4	81.1	601	4	US-09-949-016-41096
16	15.4	81.1	858	3	US-09-314-938-12
17	15.4	81.1	909	4	US-09-252-991A-7481
18	15.4	81.1	1149	4	US-09-252-991A-7156
19	15.4	81.1	1335	4	US-09-252-991A-7421
20	15.4	81.1	2667	4	US-09-252-991A-7216
21	15.4	81.1	16073	4	US-09-949-016-12905
22	15.4	81.1	16073	4	US-09-949-016-12905
23	15.4	81.1	45862	4	US-09-949-016-13928
24	15.4	81.1	102008	4	US-09-949-016-16617
25	15	78.9	396	4	US-09-513-999C-13741
26	15	78.9	855	4	US-09-949-016-1607
27	15	78.9	855	4	US-09-949-016-1608

28	15	78.9	7130	3	US-09-056-105-31	Sequence 31, Appl
29	15	78.9	9245	4	US-09-949-016-13349	Sequence 13349, A
30	15	78.9	9245	4	US-09-949-016-13350	Sequence 13350, A
31	15	78.9	42741	4	US-09-949-016-11857	Sequence 11857, A
32	15	78.9	150394	4	US-09-949-016-13042	Sequence 13042, A
33	14.8	77.9	65	1	US-08-105-483-124	Sequence 124, App
34	14.8	77.9	65	1	US-07-714-687-37	Sequence 37, Appl
35	14.8	77.9	65	1	US-08-224-391-37	Sequence 37, Appl
36	14.8	77.9	65	1	US-08-464-304-37	Sequence 37, Appl
37	14.8	77.9	65	1	US-08-709-209-124	Sequence 124, App
38	14.8	77.9	65	1	US-08-458-101-124	Sequence 124, App
39	14.8	77.9	69	1	US-08-105-483-123	Sequence 123, App
40	14.8	77.9	69	1	US-07-714-687-36	Sequence 36, Appl
41	14.8	77.9	69	1	US-08-224-391-36	Sequence 36, Appl
42	14.8	77.9	69	1	US-08-464-304-36	Sequence 36, Appl
43	14.8	77.9	69	1	US-08-709-209-123	Sequence 123, App
44	14.8	77.9	69	1	US-08-458-101-123	Sequence 123, App
45	14.8	77.9	117	1	US-08-239-498A-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-08-971-244-1
Sequence 1, Application US/08971244
Patent No. 5897179
GENERAL INFORMATION:
APPLICANT: Cohen, Lucy
APPLICANT: Baerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,244
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3996
US-08-971-244-1
Query Match: 100.0%; Score 19; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0

Db 1979 GCCAGTGTTCCTGAG 1997

RESULT 2

US-09-286-891-1

Sequence 1, Application US/09286891

Patent No. 6172195

GENERAL INFORMATION:

APPLICANT: Cohen, Lucy

APPLICANT: Baerle, Patrick

TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/286,891

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/971,244

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3999 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3996

US-09-286-891-1

Query Match 100.0%; Score 19; DB 3; Length 3999;

Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTTCCTGAG 19

Db 1979 GCCAGTGTTCCTGAG 1997

RESULT 3

US-09-949-016-68848

Sequence 68848, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68848

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-68848

Query Match 83.2%; Score 15.8; DB 4; Length 601;

Best Local Similarity 89.5%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGTGTTCCTGAG 19

Db 240 GCCAGTGTTCCTGAG 258

RESULT 4

US-09-949-016-68849

Sequence 68849, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68849

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-68849

Query Match 83.2%; Score 15.8; DB 4; Length 601;

Best Local Similarity 89.5%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGTGTTCCTGAG 19

Db 91 GCCAGTGTTCCTGAG 109

RESULT 5

US-09-018-584A-28/c

Sequence 28, Application US/09018584A

Patent No. 623863

GENERAL INFORMATION:

APPLICANT: Schumm, James W.

APPLICANT: Baerle, Patrick

TITLE OF INVENTION: MATERIALS AND METHODS FOR

TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Promega Corporation

STREET: 2800 Woods Hollow Road

CITY: Madison

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53711-5399

COMPUTER READABLE FORM:

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68848

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-68848

Query Match 83.2%; Score 15.8; DB 4; Length 601;

Best Local Similarity 89.5%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGTGTTCCTGAG 19

Db 240 GCCAGTGTTCCTGAG 258

RESULT 4

US-09-949-016-68849

Sequence 68849, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68849

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-68849

Query Match 83.2%; Score 15.8; DB 4; Length 601;

Best Local Similarity 89.5%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGTGTTCCTGAG 19

Db 91 GCCAGTGTTCCTGAG 109

RESULT 5

US-09-018-584A-28/c

Sequence 28, Application US/09018584A

Patent No. 623863

GENERAL INFORMATION:

APPLICANT: Schumm, James W.

APPLICANT: Baerle, Patrick

TITLE OF INVENTION: MATERIALS AND METHODS FOR

TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Promega Corporation

STREET: 2800 Woods Hollow Road

CITY: Madison

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53711-5399

COMPUTER READABLE FORM:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 16:38:33 ; Search time 193.988 Seconds
(without alignments)
633.931 Million cell updates/sec

Title: US-10-041-856-82

Perfect score: 19
Sequence: 1 gccagctgttttcctgag 19

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications NA:*

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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	100.0	201	US-10-719-993-4501	Sequence 4501, Ap
3	19	100.0	201	US-10-719-993-4507	Sequence 4507, Ap
4	19	100.0	201	US-10-719-993-4528	Sequence 4528, Ap
5	19	100.0	201	US-10-719-993-4534	Sequence 4534, Ap
6	19	100.0	201	US-10-719-993-4557	Sequence 4557, Ap
7	19	100.0	201	US-10-719-993-4563	Sequence 4563, Ap

8	19	100.0	201	20	US-10-719-993-4587	Sequence 4587, Ap
9	19	100.0	201	20	US-10-719-993-4592	Sequence 4592, Ap
10	19	100.0	201	20	US-10-719-993-4614	Sequence 4614, Ap
11	19	100.0	201	20	US-10-719-993-4620	Sequence 4620, Ap
12	19	100.0	201	20	US-10-719-993-34840	Sequence 34840, A
13	19	100.0	201	20	US-10-719-993-34842	Sequence 34842, A
14	19	100.0	201	20	US-10-719-993-34877	Sequence 34877, A
15	19	100.0	201	20	US-10-719-993-34940	Sequence 34940, A
16	19	100.0	4256	20	US-10-719-993-319	Sequence 319, App
17	19	100.0	4803	10	US-09-930-213-276	Sequence 276, App
18	19	100.0	4803	21	US-10-956-157-11094	Sequence 1094, App
19	19	100.0	5840	20	US-10-719-993-322	Sequence 322, App
20	19	100.0	5924	13	US-10-041-856-2	Sequence 2, Appl1
21	19	100.0	5957	20	US-10-719-993-320	Sequence 320, App
22	19	100.0	6107	20	US-10-719-993-321	Sequence 321, App
23	19	100.0	6179	20	US-10-719-993-318	Sequence 318, App
24	19	100.0	66479	13	US-10-041-856-1	Sequence 1, Appl1
25	19	100.0	78878	20	US-10-719-993-6863	Sequence 6863, App1
26	18	94.7	392	10	US-09-930-213-71	Sequence 71, Appl1
27	17.4	91.6	656	13	US-10-027-632-44690	Sequence 44690, A
28	17.4	91.6	656	17	US-10-027-632-44690	Sequence 44690, A
29	16.4	86.3	482	20	US-10-723-860-4189	Sequence 4189, App
30	16.4	86.3	14117	20	US-10-482-936-1	Sequence 1, Appl1
31	16.4	86.3	14117	20	US-10-482-936-3	Sequence 3, Appl1
32	16.4	86.3	3186778	13	US-10-027-632-174961	Sequence 174961, Sequence 174961,
33	16.4	86.3	3186778	17	US-10-027-632-174961	Sequence 8725, Ap
34	16	84.2	432	9	US-09-960-352-8725	Sequence 22, Appl
35	16	84.2	770	9	US-09-966-881-22	Sequence 40898, A
36	15.8	83.2	189	17	US-10-242-535A-40898	Sequence 40898, A
37	15.8	83.2	189	18	US-10-085-783A-40898	Sequence 3334, Ap
38	15.8	83.2	203	14	US-10-066-543-3334	Sequence 12632, A
39	15.8	83.2	467	18	US-10-424-599-12632	Sequence 57294, A
40	15.8	83.2	473	17	US-10-242-535A-57294	Sequence 57294, A
41	15.8	83.2	473	18	US-10-085-783A-57294	Sequence 57294, A
42	15.8	83.2	480	17	US-10-242-535A-56824	Sequence 56824, A
43	15.8	83.2	480	18	US-10-085-783A-56824	Sequence 56824, A
44	15.8	83.2	594	17	US-10-042-535A-46356	Sequence 46356, A
45	15.8	83.2	594	18	US-10-085-783A-46356	Sequence 46356, A

ALIGNMENTS

RESULT 1
US-10-041-856-82
Sequence 82, Application US/10041856
Publication No. US20020169299A1
GENERAL INFORMATION:
APPLICANT: SIAUGENHAUPT, SUSAN
TITLE OF INVENTION: GUSELLA, JAMES F
TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
FILE REFERENCE: 1829-4004US1
CURRENT APPLICATION NUMBER: US/10/041, 856
CURRENT FILING DATE: 2002-07-08
PRIORITY FILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 82
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-041-856-82

Query Match 100.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GCCAGCTGTTTTCCTGAG 19
|||||

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Db      1 GCCAGTGTTCCTGAG 19

RESULT 2
US-10-719-993-4501
; Sequence 4501, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4501
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4501

Query Match      100.0%; Score 19; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GCCAGTGTTCCTGAG 19
        |||||||
Db      154 GCCAGTGTTCCTGAG 172

RESULT 3
US-10-719-993-4507
; Sequence 4507, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4507
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4507

Query Match      100.0%; Score 19; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GCCAGTGTTCCTGAG 19
        |||||||
Db      115 GCCAGTGTTCCTGAG 133

RESULT 4
US-10-719-993-4528
; Sequence 4528, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4528
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; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4528

Query Match      100.0%; Score 19; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GCCAGTGTTCCTGAG 19
        |||||||
Db      154 GCCAGTGTTCCTGAG 172

RESULT 5
US-10-719-993-4534
; Sequence 4534, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4534
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4534

Query Match      100.0%; Score 19; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GCCAGTGTTCCTGAG 19
        |||||||
Db      115 GCCAGTGTTCCTGAG 133

RESULT 6
US-10-719-993-4557
; Sequence 4557, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4557
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4557

Query Match      100.0%; Score 19; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GCCAGTGTTCCTGAG 19
        |||||||
Db      154 GCCAGTGTTCCTGAG 172

RESULT 7
US-10-719-993-4563
; Sequence 4563, Application US/10719993
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 930.414 Seconds
(without alignments)
777.311 Million cell updates/sec

Title: US-10-041-856-82

Perfect score: 19

Sequence: 1 gccagctgtcttcgtcctgag 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : EST:*

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2: gb_ests2:*

3: gb_hcc:*

4: gb_esc3:*

5: gb_esc4:*

6: gb_esc5:*

7: gb_esc6:*

8: gb_ests1:*

9: gb_esc2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	19	100.0	412	2	BF742852 IL2-BT073
c 2	19	100.0	417	7	CN256146 170005321
c 3	19	100.0	447	2	BF840993 RC3-HT097
c 4	19	100.0	513	1	AL702133 DKFp686G
c 5	19	100.0	553	4	BM512007 1j77d11.x
c 6	19	100.0	580	5	BP243833 BP243833
c 7	19	100.0	618	4	BC395601 602458222
c 8	19	100.0	709	7	CN256149 170004241
c 9	19	100.0	874	5	BU156074 AGENCOURT
c 10	19	100.0	911	4	BE256729 601115546
c 11	19	100.0	931	4	BC286503 602382995
c 12	19	100.0	1134	4	CN641971 ILLUMIGEN
c 13	19	100.0	3833	3	CR749385 Homo sapi
c 14	19	100.0	3999	9	AY144501 Homo sapi
c 15	19	100.0	3999	9	AY144502 Homo sapi
c 16	18	94.7	595	1	AA324126 Pan trogl
c 17	18	94.7	595	1	AA324126 EST77019
c 18	17.4	91.6	607	7	CF608263 GEMMA01.0
c 19	17.4	91.6	607	7	BP1717388 BP1717388
c 20	17.4	91.6	647	7	CK883346 SGP167202
c 21	17.4	91.6	672	6	CB511829 Bsal19B54
c 22	17.4	91.6	713	6	CK833783 4057942 B
c 23	17.4	91.6	852	6	CB198332 AGENCOURT
c 24	17.4	91.6	856	6	CD325659 AGENCOURT

c 25	17.4	91.6	911	9	CU263184 ZMMBB062
c 26	17.4	91.6	997	9	CNS04WSC
c 27	17	89.5	424	7	CO883709 Boven12
c 28	17	89.5	435	1	AL960247 AL960247
c 29	17	89.5	477	8	B2934659 CH240_90H
c 30	17	89.5	533	1	AL776870 AL776870
c 31	17	89.5	553	8	AO879770 HS 4821 A
c 32	17	89.5	633	7	CR955068 4055153_B
c 33	17	89.5	658	7	CN794326 4129481 B
c 34	17	89.5	667	7	CC770787 CR706818
c 35	17	89.5	743	9	CR796818 GR0AAA15A
c 36	17	89.5	780	9	CR816573 GR0AAA11B
c 37	17	89.5	899	8	BZ862322 CH240_286
c 38	17	89.5	1045	9	CU093512 ISB1-23K3
c 39	16.4	86.3	164	9	CC518828 CH240_365
c 40	16.4	86.3	171	8	BZ881702 CH240_241
c 41	16.4	86.3	182	9	CC480699 CH240_308
c 42	16.4	86.3	371	9	CR833829 GR0AAA67C
c 43	16.4	86.3	404	9	CC763977 CH240_410
c 44	16.4	86.3	425	1	AA080454 mn98C05.r
c 45	16.4	86.3	429	8	BZ908709 CH240_98M

ALIGNMENTS

RESULT 1
BF742852/c 412 bp mRNA linear EST 10-JAN-2001
LOCUS IL2-BT0734-041000-178-C01 BT0734 Homo sapiens CDNA, mRNA sequence.
DEFINITION BF742852
ACCESSION BF742852.1 GI:12069528
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-BT0734-041000-178-C01&t3=2000-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 410.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/def_stage="Adult"
/clone_id="BT0734"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTGTTTGCTGAG 19
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Db 100 GCCAGTGTGTTTGCTGAG 82

RESULT 2
LOCUS CN256146 417 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532188935 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
ACCESSION CN256146
VERSION CN256146.1 GI:47272560
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 417)
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalian, R., Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 417 Std Error: 0.00.
Location/Qualifiers

TITLE
JOURNAL
COMMENT

FEATURES
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1. .417
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/mol_type="mRNA"
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/clone_id="GRN_ES"
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ORIGIN

Query Match 100.0%; Score 19; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTGTTTGCTGAG 19
|||||
Db 83 GCCAGTGTGTTTGCTGAG 101

RESULT 3
LOCUS BF840993/c 447 bp mRNA linear EST 13-JAN-2001
DEFINITION RC3-HT0974-011200-013-a03 HT0974 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF840993
VERSION BF840993.1 GI:12193641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 447)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=RC3&t2=RC3-HT0974-011200-013-a03&t3=200-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 29
High quality sequence stop: 447.
Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_id="HT0974"
/note="Organ: head_neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGTGTGTTTGCTGAG 19
|||||
Db 420 GCCAGTGTGTTTGCTGAG 402

RESULT 4
LOCUS AL702133 513 bp mRNA linear EST 04-SEP-2003
DEFINITION DFFZ686G02155_r1 686 (synonym: hlc3) Homo sapiens CDNA clone DFFZ686G02155 5', mRNA sequence.
ACCESSION AL702133
VERSION AL702133.1 GI:19685488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 513)
Bloeker, H., Boecher, M., Brandt, P., Mewes, W., Weill, B. and Wiemann, S.

TITLE EST (Bloeker, H., Boecher, M., Brandt, P., Mewes, H.W., Weill, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:44:02 ; Search time 546.895 Seconds

(without alignments)
1683.411 Million cell updates/sec

Title: US-10-041-856-83

Perfect score: 19
Sequence: 1 cggattgtcactgtgtgc 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_hbg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	AX676130 Sequence
2	19	100.0	803	6	BD147310 Primer fo
3	19	100.0	803	6	AX867248 Sequence
4	19	100.0	2471	6	BD157787 Primer fo
5	19	100.0	2471	6	AX879348 Sequence
6	19	100.0	2471	6	AX022559 Homo sapi
7	19	100.0	3516	6	CO724004 Sequence
8	19	100.0	3999	6	AR070165 Sequence
9	19	100.0	3999	6	AR124807 Sequence
10	19	100.0	4417	6	CQ850139 Sequence
11	19	100.0	4417	6	AX127237 Homo sapi
12	19	100.0	4788	6	BD156525 Primer fo
13	19	100.0	4788	6	AX877177 Sequence
14	19	100.0	4788	6	AX001641 Homo sapi
15	19	100.0	4803	6	BD171366 Method fo
16	19	100.0	4803	6	BD173600 Method of
17	19	100.0	4803	6	AX210634 Sequence
18	19	100.0	4803	9	AF044195 Homo sapi
19	19	100.0	5047	9	BC033094 Homo sapi

20	19	100.0	5924	6	AX676049 Sequence
21	19	100.0	5924	6	AF153419 Homo sapi
22	19	100.0	66479	6	AX676048 Sequence
23	19	100.0	78376	9	AL359692 Human DNA
24	17.4	91.6	4347	4	AF388202 Oryctolag
25	17.4	91.6	166062	2	AC146313 Pongo pyg
26	17.4	91.6	176547	9	AC092447 Homo sapi
27	17.4	91.6	184062	9	AC149232 Pan trogl
28	17.4	91.6	191966	9	AC150280 Pan trogl
29	17	89.5	151559	9	AL390294 Human DNA
30	17	89.5	190891	2	AC058800 Homo sapi
31	16.4	86.3	3644	14	LN3685 Hantavirus
32	16.4	86.3	25057	2	SPCP1E11 S.pombe c
33	16.4	86.3	97057	2	AL627344 Human DNA
34	16.4	86.3	111363	9	AC008606 Homo sapi
35	16.4	86.3	116730	9	AC008548 Homo sapi
36	16.4	86.3	151301	2	AL354717 Homo sapi
37	16.4	86.3	156764	2	AC135268 Rattus no
38	16.4	86.3	163781	9	AC058784 Homo sapi
39	16.4	86.3	163910	5	AC145802 Xenopus t
40	16.4	86.3	166950	9	AC113414 Homo sapi
41	16.4	86.3	167227	2	CR759866 Dantio rer
42	16.4	86.3	168666	2	AC131085 Mus muscu
43	16.4	86.3	168874	10	AC132135 Mus muscu
44	16.4	86.3	170141	2	AC015479 Homo sapi
45	16.4	86.3	172192	9	AC091921 Homo sapi

ALIGNMENTS

RESULT 1
AX676130
LOCUS AX676130 19 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 83 from Patent WO2059381.
ACCESSION AX676130
VERSION AX676130.1 GI:29333814
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Slangenhuysen, S. and Guesella, J.F.
TITLE Gene for identifying individuals with familial dysautonomia
JOURNAL Patent: WO 02059381-A 83 01-AUG-2002;
The General Hospital Corporation (US)
FEATURES
source location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGATTGTCACTGTGTGC 19
DB 1 CGGATTGTCACTGTGTGC 19
RESULT 2
LOCUS BD147310 803 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD147310.1 GI:27853068
VERSION BD147310.1
KEYWORDS UP 2002191363-A/2153.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 803)
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ihii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 2153 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/2153
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
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Primer for synthesizing full-length cDNA and use thereof FH Key
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ORIGIN
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DEFINITION Sequence 2153 from Patent EP1074617.
ACCESSION AX867248
VERSION AX867248.1 GI:40021619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ihii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 2153 07-FEB-2001;
Research Association for Biotechnology (JP)
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 78 CGGATTGTCACGTGTGTC 96
RESULT 4

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LOCUS BD157787 2471 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD157787
VERSION BD157787.1 GI:27863545
KEYWORDS JP 2002191363-A/12630.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2471)
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ihii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 12630 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/12630
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
10, C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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RESULT 5
LOCUS AX879348 2471 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 14253 from Patent EP1074617.
ACCESSION AX879348
VERSION AX879348.1 GI:40034084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ihii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 14253 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES Location/Qualifiers
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 09:42:59 ; Search time 134.525 Seconds
(without alignments)
836.092 Million cell updates/sec

Title: US-10-041-856-83

Perfect score: 19
Sequence: 1 cggatctgctactgtctgtgc 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	100.0	3999	AAK28025	AAK28025 Human IKA
5	19	100.0	3999	AAK29756	AAK29756 Human IKA
6	19	100.0	4417	ADR07102	ADR07102 Full leng
7	19	100.0	4788	AAH14533	AAH14533 Human dlf
8	19	100.0	4803	AAH81767	AAH81767 Human I-k
9	19	100.0	4803	AAH44190	AAH44190 Human I-k
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12	19	100.0	66479	ABQ80566	ABQ80566 Human IKB
13	19	100.0	66479	ABQ80565	ABQ80565 Human IKB
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15	17.4	91.6	66479	ABQ80567	ABQ80567 Mutant hu
16	17.4	91.6	66479	ABQ80568	ABQ80568 Mutant hu
17	16.4	86.3	28564	ADBE6369	ADBE6369 Human gen
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19	15.8	83.2	1296	AAH84042	AAH84042 DNA encod
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23	15.8	83.2	3616	4	ABL04189	ABL04189 Drosophila
24	15.8	83.2	7091	4	ABL04188	ABL04188 Drosophila
25	15.8	83.2	90583	8	ACD13447	ACD13447 Human DNA
26	15.8	83.2	349980	5	AAH68525	AAH68525 C glutami
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28	15.4	81.1	543	10	ADD34882	ADD34882 Mouse mit
29	15.4	81.1	592	13	ACN60285	ACN60285 Cotton gy
30	15.4	81.1	752	10	ADF55277	ADF55277 SINE fam1
31	15.4	81.1	1067	13	ADR62195	ADR62195 Cotton CD
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34	15.4	81.1	2682	8	ACA50396	ACA50396 Proteobact
35	15.4	81.1	3350	10	ABT42379	ABT42379 Toxicity
36	15.4	81.1	5960	6	ABK12735	ABK12735 Human int
37	15.4	81.1	5961	2	AAQ74060	AAQ74060 Human int
38	15.4	81.1	5961	12	ACF57525	ACF57525 Human IFN
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ALIGNMENTS

RESULT 1
ABQ80559 standard; DNA, 19 BP.
ABQ80559:
08-NOV-2002 (first entry)
IKBKAP PCR primer 19F.
Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
PCR; primer; ss.
Homo sapiens.
W0200259381-A2.
01-AUG-2002.
07-JAN-2002; 2002WO-US000473.
06-JAN-2001; 2001US-026080P.
(GEHO) GEN HOSPITAL CORP.
Slaugenhaup S, Guseella JF;
WPI; 2002-674806/72.
New IKBKAP genes with mutations, useful for identifying a subject with
familial dysautonomia (FD), or for rapid carrier screening in the
Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
prenatal diagnosis.
Claim 33; Page 27; 109pp; English.
The present invention relates to methods and compositions useful for
detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM
223900). It was found that mutations in the IKBKAP gene (see ABQ80565)
are associated with FD. The mutation associated with the major haplotype
of FD, FDI mutation, is a base pair (bp) mutation, where the thymine

CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from PD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, PD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKKAP nucleic acid sequences are useful for
CC identifying a subject with PD and for rapid carrier screening. The IKKAP
CC gene maps to chromosome 9p31. PCR primers ABQ80558-ABQ80560 were used to
CC detect the splicing defect in IKKAP gene
CC
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SQ Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CGGATTGTCACGTGTGTC 19
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AC AAH05318;
XX
DT 26-JUN-2001 (first entry)
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DE Human cDNA clone (5'-primer) SEQ ID NO:2153.
XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN BP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
XX
PR 27-AUG-1999; 99JP-00300253.
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PR 11-JAN-2000; 2000JP-00118776.
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PR 02-MAY-2000; 2000JP-00183767.
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PR 09-JUN-2000; 2000JP-00241899.
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PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
XX
PI Iehii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX
PT length cDNAs defined in the specification, and for the detection and/or
XX
PT diagnosis of the abnormality of the proteins encoded by the full-length
XX
PT cDNAs.
XX
PS Claim 1; SEQ ID NO 2153; 2537bp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX
XX length cDNAs defined in the specification. Where a primer set comprises:
XX
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX
XX complementary strand of a polynucleotide which comprises one of the 5602
XX
XX nucleotide sequences defined in the specification, where the
XX
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX
XX of an oligonucleotide comprising a sequence complementary to the
XX
XX complementary strand of a polynucleotide which comprises a 5'-end
XX
XX sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences, and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
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Query Match 100.0%; Score 19; DB 4; Length 803;
Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CGGATTGTCACGTGTGTC 19
Db 78 CGGATTGTCACGTGTGTC 96
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AC AAH15795;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14253.
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KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN BP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
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PR 29-JUL-1999; 99JP-00248036.
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PR 27-AUG-1999; 99JP-00300253.
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PR 11-JAN-2000; 2000JP-00118776.
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PR 02-MAY-2000; 2000JP-00183767.
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PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
XX
PI Iehii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX
PT length cDNAs defined in the specification, and for the detection and/or
XX
PT diagnosis of the abnormality of the proteins encoded by the full-length
XX
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14253; 2537bp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX
XX length cDNAs defined in the specification. Where a primer set comprises:
XX
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX
XX complementary strand of a polynucleotide which comprises one of the 5602
XX
XX nucleotide sequences defined in the specification, where the
XX
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX
XX of an oligonucleotide comprising a sequence complementary to the
XX
XX complementary strand of a polynucleotide which comprises a 5'-end

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:57:07 ; Search time 39.2901 Seconds
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791.274 Million cell updates/sec

Title: US-10-041-856-83

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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13	15	78.9	601	4	US-09-949-016-74148
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24	14.8	77.9	601	4	US-09-949-016-35277
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C 32	14.8	77.9	741	4	US-09-305-839-2	Sequence 2, Appli
C 33	14.8	77.9	797	2	US-08-739-485-2	Sequence 64, Appli
C 34	14.8	77.9	797	4	US-09-016-434-64	Sequence 7, Appli
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C 42	14.8	77.9	5040	4	US-09-949-016-16394	Sequence 16120, A
C 43	14.8	77.9	15069	4	US-09-949-016-16120	Sequence 12631, A
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ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/08971244
; Patent No. 5891719
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baueerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971.244
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: 797-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
; US-08-971-244-1

Query Match 100.0%; Score 19; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2086 CGGATTGTCACTGTGTGC 2104

RESULT 2

US-09-286-891-1
Sequence 1, Application US/09286891
Patent No. 6172195
GENERAL INFORMATION:
APPLICANT: Cohen, Lucy
APPLICANT: Baerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/286,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,244
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3996
US-09-286-891-1

Query Match 100.0%; Score 19; DB 3; Length 3999;
Best Local Similarity 100.0%; Pred. No. 2,6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGATTGTCACTGTGTGC 19

Db 2086 CGGATTGTCACTGTGTGC 2104

RESULT 3

US-09-270-767-11478/c
Sequence 11478, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11478
LENGTH: 1839

TYPE: DNA
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: n means any nucleotide
US-09-270-767-11478

Query Match 83.2%; Score 15.8; DB 4; Length 1839;
Best Local Similarity 89.5%; Pred. No. 1,1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGATTGTCACTGTGTGC 19

Db 1366 CGGATTGTCACTGTGTGC 1348

RESULT 4

US-09-602-787A-577
Sequence 577, Application US/09602787A
Patent No. 6696561
GENERAL INFORMATION:
APPLICANT: Pompeius, Mark
APPLICANT: Krüger, Burkhard
APPLICANT: Schöler, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habermeyer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 16:38:33 ; Search time 193.988 Seconds
(without alignments)
633.931 Million cell updates/sec

Title: US-10-041-856-83

Perfect score: 19
Sequence: 1 cggatgtcactgtgtgfc 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19.100.0	4803	21	US-10-955-157-1094	Sequence 1094, Ap
4	19.100.0	5924	13	US-10-041-856-2	Sequence 2, Appl1
5	19.100.0	66479	13	US-10-041-856-1	Sequence 4499, Ap
6	18.6	97.9	201	US-10-719-993-4499	Sequence 4527, Ap
7	18.6	97.9	201	US-10-719-993-4527	Sequence 4527, Ap

8	18.6	97.9	201	20	US-10-719-993-4556	Sequence 4556, Ap
9	18.6	97.9	201	20	US-10-719-993-4585	Sequence 4585, Ap
10	18.6	97.9	201	20	US-10-719-993-4613	Sequence 4613, Ap
11	18.6	97.9	201	20	US-10-719-993-34955	Sequence 34955, A
12	18.6	97.9	4256	20	US-10-719-993-319	Sequence 319, App
13	18.6	97.9	5840	20	US-10-719-993-322	Sequence 322, App
14	18.6	97.9	5957	20	US-10-719-993-320	Sequence 320, App
15	18.6	97.9	6107	20	US-10-719-993-321	Sequence 321, App
16	18.6	97.9	6179	20	US-10-719-993-318	Sequence 318, App
17	18.6	97.9	78878	20	US-10-719-993-6863	Sequence 6863, App
18	18.6	97.9	19	21	US-10-913-280-548	Sequence 548, App
19	17.4	91.6	21	21	US-10-913-280-549	Sequence 549, App
20	17.4	89.5	18	21	US-10-913-280-123	Sequence 123, App
21	16	84.2	600	22	US-10-972-079-73099	Sequence 73099, A
22	16	84.2	616	22	US-10-767-701-1312	Sequence 1312, Ap
23	15.8	83.2	412	22	US-10-572-079-20615	Sequence 20615, A
24	15.8	83.2	2544	9	US-09-738-626-488	Sequence 488, App
25	15.8	83.2	2733	18	US-10-627-476-577	Sequence 577, App
26	15.8	83.2	3309400	9	US-09-738-626-1	Sequence 75776, A
27	15.4	81.1	408	20	US-10-425-115-75776	Sequence 3993, Ap
28	15.4	81.1	474	13	US-10-027-632-3993	Sequence 3993, Ap
29	15.4	81.1	474	13	US-10-027-632-3994	Sequence 3994, Ap
30	15.4	81.1	474	13	US-10-027-632-3995	Sequence 3995, Ap
31	15.4	81.1	474	17	US-10-027-632-3993	Sequence 3993, Ap
32	15.4	81.1	474	17	US-10-027-632-3994	Sequence 3994, Ap
33	15.4	81.1	474	17	US-10-027-632-3995	Sequence 3995, Ap
34	15.4	81.1	592	19	US-10-021-323-15066	Sequence 15066, A
35	15.4	81.1	638	18	US-10-425-114-35933	Sequence 35933, A
36	15.4	81.1	749	19	US-10-437-963-56184	Sequence 56184, A
37	15.4	81.1	1067	19	US-10-767-795-2976	Sequence 2976, Ap
38	15.4	81.1	1800	9	US-09-974-300-1667	Sequence 1667, Ap
39	15.4	81.1	2682	17	US-10-282-122A-38266	Sequence 38266, A
40	15.4	81.1	2694	18	US-10-425-114-31868	Sequence 31868, A
41	15.4	81.1	2804	20	US-10-425-115-20896	Sequence 20896, A
42	15.4	81.1	2976	20	US-10-425-115-116362	Sequence 116362, A
43	15.4	81.1	3350	18	US-10-152-319A-2081	Sequence 2081, Ap
44	15.4	81.1	5961	17	US-10-429-802-35	Sequence 35, Appl1
45	15.4	81.1	5961	17	US-10-430-503-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1
US-10-041-856-83
Sequence 83, Application US/10041856
Publication No. US20020169299A1
GENERAL INFORMATION:
APPLICANT: SLAUGENHAUPT, SUSAN
APPLICANT: GUSELLA, JAMES F.
TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
TITLE OF INVENTION: DYSATONOMIA
FILE REFERENCE: 1829-4004US1
CURRENT APPLICATION NUMBER: US/10/041.856
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 60/260,080
PRIOR FILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 83
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-041-856-83

Query Match 100.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. NO. 5.3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CGGATGTCTACTGTGTGTC 19
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Db 1 CGATTGTCACGTGTGTC 19

RESULT 2

US-09-930-213-276

Sequence 276, Application US/09910213

Publication No. US20030170625A1

GENERAL INFORMATION:

APPLICANT: ROSENTHAL, ANDRE

APPLICANT: HINZMANN, BERND

APPLICANT: SCHAFER, REINHARD

APPLICANT: ZUBER, JOHANNES

APPLICANT: TCHÉ-NITSE, OLEG

APPLICANT: GRIPS, MARTIN

APPLICANT: HELLMGEL, MARTIN

APPLICANT: SCHMITZ, ANNE-CHANTAL

APPLICANT: SEES, CHRISTINE

TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS

FILE REFERENCE: ALBRE-14

CURRENT APPLICATION NUMBER: US/09/930.213

CURRENT FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: DE 10004102.7

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 885

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 276

LENGTH: 4803

TYPE: DNA

ORGANISM: Homo sapiens

US-09-930-213-276

Query Match 100.0%; Score 19; DB 10; Length 4803;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGATTGTCACGTGTGTC 19

Db 2389 CGATTGTCACGTGTGTC 2407

RESULT 3

US-10-956-157-1094

Sequence 1094, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956.157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 1094

LENGTH: 4803

TYPE: DNA

ORGANISM: Homo sapiens

US-10-956-157-1094

Query Match 100.0%; Score 19; DB 21; Length 4803;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGATTGTCACGTGTGTC 19

Db 2389 CGATTGTCACGTGTGTC 2407

RESULT 4

US-10-041-856-2

Sequence 2, Application US/10041856

Publication No. US20020169299A1

GENERAL INFORMATION:

APPLICANT: SLAUGENHAUPT, SUSAN

APPLICANT: GUSELLA, JAMES F.

TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL

FILE REFERENCE: 1829-4004U51

CURRENT APPLICATION NUMBER: US/10/041.856

CURRENT FILING DATE: 2002-07-08

PRIOR APPLICATION NUMBER: 60/260,080

PRIOR FILING DATE: 2001-01-06

NUMBER OF SEQ ID NOS: 88

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 5924

TYPE: DNA

ORGANISM: Homo sapiens

US-10-041-856-2

Query Match 100.0%; Score 19; DB 13; Length 5924;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGATTGTCACGTGTGTC 19

Db 2396 CGATTGTCACGTGTGTC 2414

RESULT 5

US-10-041-856-1

Sequence 1, Application US/10041856

Publication No. US20020169299A1

GENERAL INFORMATION:

APPLICANT: SLAUGENHAUPT, SUSAN

APPLICANT: GUSELLA, JAMES F.

TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL

FILE REFERENCE: 1829-4004U51

CURRENT APPLICATION NUMBER: US/10/041.856

CURRENT FILING DATE: 2002-07-08

PRIOR APPLICATION NUMBER: 60/260,080

PRIOR FILING DATE: 2001-01-06

NUMBER OF SEQ ID NOS: 88

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 66479

TYPE: DNA

ORGANISM: Homo sapiens

US-10-041-856-1

Query Match 100.0%; Score 19; DB 13; Length 66479;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGATTGTCACGTGTGTC 19

Db 33713 CGATTGTCACGTGTGTC 33731

RESULT 6

US-10-719-993-4499

Sequence 4499, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CU001496

CURRENT APPLICATION NUMBER: US/10/719.993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4499

LENGTH: 201

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 930.414 Seconds
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777.311 Million cell updates/sec

Title: US-10-041-856-83

Perfect score: 19

Sequence: 1 CGAGTGTGCTGCTGTGTC 19

Scoring table: IDENTITY_NUC

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	19	100.0	580	5	BP243833 BP243833
6	19	100.0	603	5	BK478139 DKF2p666B
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8	19	100.0	641	5	BQ807986 NISC_Kk12
9	19	100.0	709	7	CN256149 170004241
10	19	100.0	803	1	AU124100 AU124100
11	19	100.0	866	5	BUS08979 AGENCOURT
12	19	100.0	874	5	BUS16074 AGENCOURT
13	19	100.0	911	2	BE256729 601115546
14	19	100.0	931	4	BC286503 602382995
15	19	100.0	931	7	CN641971 TLDMIGEN
16	19	100.0	1134	7	CN641971 TLDMIGEN
17	19	100.0	3833	3	CR749385 Homo sapi
18	19	100.0	3999	9	AY414501 Homo sapi
19	19	100.0	3999	7	AY414502 Pan trogl
20	19	89.5	442	7	CN958766 6266 1001
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22	17	89.5	703	4	BM657393 tigr-g88-
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27	16.4	86.3	514	2	CC678317 OCUI113TV
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ALIGNMENTS

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ACCESSION	CN256146	17000532188935 GRN_ES Homo sapiens CDNA 5', mRNA sequence.	417 bp	mrna	linear	EST 16-MAY-2004
VERSION	CN256146.1	GI:47272560	417 bp	mrna	linear	EST 16-MAY-2004
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W. Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)					
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W. Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)					
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)					
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Best Local Similarity	100.0%; Pred. 60;					
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DEFINITION RC3-HT0974-011200-013-a03 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF840993
VERSION BF840993.1 GI:12193641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC3act2-RC3-HT0974-011200-013-a03&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 29
High quality sequence stop: 447.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="HT0974"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 100.0%; Score 19; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGATTGTCTACTGTTGTC 19
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Db 313 CGGATTGTCTACTGTTGTC 295

RESULT 3
LOCUS AL702133 513 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686G02155.t1.686 (synonym: hlc3) Homo sapiens cDNA clone
ACCESSION DKFZp686G02155.5, mRNA sequence.
VERSION AL702133
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 513)
AUTHORS Bioecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and Wiemann,S.
TITLE EST (Bioecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weill,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by GSF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
No si sequence available.
This clone (DKFZp686G02155) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..513
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G02155"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlc3)"
/note="Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; cDNA-collection"

ORIGIN
Query Match 100.0%; Score 19; DB 1; Length 513;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGATTGTCTACTGTTGTC 19
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Db 298 CGGATTGTCTACTGTTGTC 316

RESULT 4
LOCUS BM512007 553 bp mRNA linear EST 15-FEB-2002
DEFINITION i177d11.x1 Human insulinoma homo sapiens cDNA clone IMAGE:563805
ACCESSION BM512007
VERSION BM512007.1 GI:18683150
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS Melton,D., Brown,J., Kenly,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Breestell,J., Gradwohl,G., Clifton,S., Hillier,L., Werra,M., Pape,D., Wyllie,T., Martin,J., Blyskal,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@lohp.harvard.edu

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:44:02 ; Search time 575.679 Seconds
(without alignments)
1683.411 Million cell updates/sec

Title: US-10-041-856-84
Perfect score: 20
Sequence: 1 gactgctctcatgacatgcgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX676131 Sequence
2	20	100.0	803	6	BD147310 Primer fo
3	20	100.0	803	6	AX676131 Sequence
4	20	100.0	828	6	BD147338 Primer fo
5	20	100.0	828	6	AX676131 Sequence
6	20	100.0	2471	6	BD157787 Primer fo
7	20	100.0	2471	6	AX676131 Sequence
8	20	100.0	2471	6	AX676131 Sequence
9	20	100.0	2712	6	BD160487 Primer fo
10	20	100.0	2712	6	AX676131 Sequence
11	20	100.0	2712	6	AX676131 Sequence
12	20	100.0	3516	6	AX676131 Sequence
13	20	100.0	3516	6	AX676131 Sequence
14	20	100.0	3999	6	AX676131 Sequence
15	20	100.0	4417	6	AX676131 Sequence
16	20	100.0	4417	6	AX676131 Sequence
17	20	100.0	4788	6	AX676131 Sequence
18	20	100.0	4788	6	AX676131 Sequence
19	20	100.0	4788	9	AX676131 Sequence

C 20	20	100.0	4803	6	BD171366	BD171366 Method fo
C 21	20	100.0	4803	6	BD173600	BD173600 Method of
C 22	20	100.0	4803	6	AX210634	AX210634 Sequence
C 23	20	100.0	4803	9	AF044195	AF044195 Homo sapi
C 24	20	100.0	5047	9	BC033094	BC033094 Homo sapi
C 25	20	100.0	5924	6	AX676049	AX676049 Sequence
C 26	20	100.0	5924	6	AF153419	AF153419 Homo sapi
C 27	20	100.0	66479	6	AX676048	AX676048 Sequence
C 28	20	100.0	78376	6	AL359692	AL359692 Human DNA
C 29	16.8	84.0	50842	10	BX470225	BX470225 Mouse DNA
C 30	16.8	84.0	72302	2	AC019988	AC019988 Drosophila
C 31	16.8	84.0	81019	2	AC149536	AC149536 Xenopus t
C 32	16.8	84.0	81625	2	AC004289	AC004289 Drosophila
C 33	16.8	84.0	113715	2	AC149149	AC149149 Xenopus t
C 34	16.8	84.0	116557	9	AC107022	AC107022 Homo sapi
C 35	16.8	84.0	132642	2	AC146404	AC146404 Pan trogl
C 36	16.8	84.0	136547	2	AC134966	AC134966 Gallus ga
C 37	16.8	84.0	149335	2	AC009651	AC009651 Homo sapi
C 38	16.8	84.0	174028	2	AC067831	AC067831 Homo sapi
C 39	16.8	84.0	180389	9	AC063944	AC063944 Homo sapi
C 40	16.8	84.0	195265	3	AC012071	AC012071 Homo sapi
C 41	16.8	84.0	198390	3	AC091501	AC091501 Drosophila
C 42	16.8	84.0	222776	2	AC103448	AC103448 Rattus no
C 43	16.8	84.0	228998	2	AC112472	AC112472 Rattus no
C 44	16.8	84.0	231264	2	AC095739	AC095739 Rattus no
C 45	16.8	84.0	236723	2	AC112477	AC112477 Rattus no

ALIGNMENTS

RESULT 1	AX676131	AX676131	20 bp	DNA	linear	PAT 27-MAR-2003
LOCUS	AX676131	Sequence 84 from Patent WO02059381.				
DEFINITION	AX676131	AX676131.1 GI:29333815				
ACCESSION	AX676131					
VERSION	AX676131.1	GI:29333815				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Qy						
Db						
RESULT 2						
BD147310/c						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 803)
TITLE Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
JOURNAL Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 2153 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/2153
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SATTO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10', C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 803;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATGATCGC 20
DB 470 GACTGCTCTCATGATCGC 451

RESULT 3
AX867248/c
LOCUS AX867248 803 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 2153 from Patent EP1074617.
ACCESSION AX867248
VERSION AX867248.1 GI:40021619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
TITLE Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
JOURNAL Primers for synthesizing full-length cDNA and their use
Patent: EP 1074617-A 2153 07-FEB-2001;
Research Association for Biotechnology (JP)
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source 1..803
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 803;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATGATCGC 20
DB 470 GACTGCTCTCATGATCGC 451

RESULT 4

BD147338/c
LOCUS BD147338 828 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD147338
VERSION BD147338.1 GI:27853096
KEYWORDS JP 2002191363-A/2181.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 828)
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
TITLE Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
JOURNAL Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 2181 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/2181
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SATTO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10', C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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/organism='Homo sapiens (human)'.
FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 828;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATGATCGC 20
DB 245 GACTGCTCTCATGATCGC 226

RESULT 5
AX867276/c
LOCUS AX867276 828 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 2181 from Patent EP1074617.
ACCESSION AX867276
VERSION AX867276.1 GI:40021656
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
TITLE Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
JOURNAL Primers for synthesizing full-length cDNA and their use
Patent: EP 1074617-A 2181 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
source 1..828
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 828;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 09:42:59 ; Search time 141.605 Seconds
(without alignments)
836.092 Million cell updates/sec

Title: US-10-041-856-84

Perfect score: 20
Sequence: 1 gacgtctcatagcgcgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004as:.*
13: geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	ABQ80560	IKBAP PC
2	20	100.0	803	AAH05318	AAH05318 Human CDN
3	20	100.0	828	AAH05346	AAH05346 Human CDN
4	20	100.0	2471	AAH15795	AAH15795 Human CDN
5	20	100.0	2712	AAH18495	AAH18495 Human CDN
6	20	100.0	3999	AAK28025	AAK28025 Human IKA
7	20	100.0	4417	AAK29756	AAK29756 Human IKA
8	20	100.0	4788	AAH07102	AAH07102 Full leng
9	20	100.0	4803	AAH14533	AAH14533 Human CDN
10	20	100.0	4803	AAH1767	AAH1767 Human dif
11	20	100.0	5924	AAH44190	AAH44190 Human I-K
12	20	100.0	5924	ABQ80570	ABQ80570 Mutant hu
13	20	100.0	5924	ABQ80569	ABQ80569 Human IKB
14	20	100.0	5924	ACD13384	ACD13384 Human DNA
15	20	100.0	66479	ABQ80567	ABQ80567 Mutant hu
16	20	100.0	66479	ABQ80566	ABQ80566 Mutant hu
17	20	100.0	66479	ABQ80568	ABQ80568 Mutant hu
18	20	100.0	66479	ABQ80565	ABQ80565 Mutant hu
19	16	80.0	131680	ADP29092	ADP29092 Agrotis B
20	15.8	79.0	405	AAK96654	AAK96654 Human neu

c 21	15.8	79.0	405	AAK98147	AAK98147 Human neu
c 22	15.8	79.0	405	ABT01424	ABT01424 Human neu
c 23	15.8	79.0	405	ABT02917	ABT02917 Human neu
c 24	15.8	79.0	405	ADH77679	ADH77679 Human neu
c 25	15.8	79.0	621	ADQ52747	ADQ52747 Novel can
c 26	15.8	79.0	1035	ADK16160	ADK16160 Nanoarcha
c 27	15.8	79.0	29844	AAD46552	AAD46552 Human CMO
c 28	15.8	79.0	51615	ACMA5162	ACMA5162 Human gen
c 29	15.8	79.0	110000	AAK95240_09	Continuation (10 o
c 30	15.8	79.0	110000	AAK96733_09	Continuation (10 o
c 31	15.8	79.0	110000	ABT00010_09	Continuation (10 o
c 32	15.8	79.0	110000	ABT01503_09	Continuation (10 o
c 33	15.8	79.0	110000	ADH77486_09	Continuation (10 o
c 34	15.8	79.0	110000	ADK16049_0	Continuation (10 o
c 35	15.8	79.0	180227	ABD33268	ABD33268 Nanoarcha
c 36	15.4	77.0	527	ACN58267	ACN58267 Human can
c 37	15.4	77.0	637	ADBS1555	ADBS1555 Primary r
c 38	15.4	77.0	702	ACA27727	ACA27727 Prokaryot
c 39	15.4	77.0	1350	ACA27620	ACA27620 Prokaryot
c 40	15.4	77.0	1602	ABZ14834	ABZ14834 Arabidops
c 41	15.4	77.0	1602	ADA68575	ADA68575 Arabidops
c 42	15.4	77.0	2550	ABQ94264	ABQ94264 Iovf gene
c 43	15.4	77.0	2550	ABN79909	ABN79909 Fungal ZB
c 44	15.4	77.0	5436	AAV72895	AAV72895 Mouse UCP
c 45	15.4	77.0	5436	AAZ24193	AAZ24193 Mouse UCP

ALIGNMENTS

RESULT 1	ABQ80560	standard; DNA, 20 BP.
ID	ABQ80560	
XX	ABQ80560;	
AC	08-NOV-2002	(first entry)
DT	08-NOV-2002	
XX	IKBAP PCR primer 23R.	
DE	Human; IKBAP; Familial Dysautonomia; FD; Riley-Day syndrome;	
KW	Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;	
KM	PCR; primer; ss.	
OS	Homo sapiens.	
XX	WO200259381-A2.	
PN	01-AUG-2002.	
PD	07-JAN-2002; 2002WO-US000473.	
PF	06-JAN-2001; 2001US-0260080P.	
XX	(GHEO) GEN HOSPITAL CORP.	
PA	Slaugenhaupt S, Gusejlla JF;	
PI	WPI; 2002-674806/72.	
DR	New IKBAP genes with mutations, useful for identifying a subject with	
XX	familial dysautonomia (FD), or for rapid carrier screening in the	
PT	Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or	
PT	prenatal diagnosis.	
XX	Claim 33; Page 27; 109pp; English.	
XX	The present invention relates to methods and compositions useful for	
CC	detecting mutations which cause Familial Dysautonomia (FD, Riley-Day	
CC	syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM	
CC	223900). It was found that mutations in the IKBAP gene (see ABQ80565)	
CC	are associated with FD. The mutation associated with the major haplotype	
CC	of FD, FDI mutation, is a base pair (bp) mutation, where the thymine	

CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from PD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, R62 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKKAP nucleic acid sequences are useful for
CC identifying a subject with PD and for rapid carrier screening. The IKKAP
CC gene maps to chromosome 9q31. PCR primers ABQ80558-ABQ80560 were used to
CC detect the splicing defect in IKKAP gene

XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACTGCTCTCATAGCATCGC 20
Db 1 GACTGCTCTCATAGCATCGC 20

RESULT 2
AAH05318/c
ID AAH05318 standard; cDNA; 803 BP.

XX
AC AAH05318;

XX
DT 26-JUN-2001 (first entry)

XX
DE Human cDNA clone (5'-primer) SEQ ID NO:2153.

XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX
OS Homo sapiens.

XX
PN EPI074617-A2.

XX
PD 07-FEB-2001.

XX
PF 28-JUL-2000; 2000EP-00116126.

XX
PR 29-JUN-1999; 99JP-00248036.

XX
PR 27-AUG-1999; 99JP-00300253.

XX
PR 11-JAN-2000; 2000JP-00118776.

XX
PR 02-MAY-2000; 2000JP-00183767.

XX
PR 09-JUN-2000; 2000JP-00241899.

XX
PA (HELI-) HELIX RES INST.

XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Iehli S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.

XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

XX
PS Claim 1; SEQ ID NO 2153; 2537bp + Sequence Listing; English.

XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX length cDNAs defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination
CC of the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX
SQ Sequence 803 BP; 251 A; 154 C; 172 G; 222 T; 0 U; 4 Other;

Query Match 100.0%; Score 20; DB 4; Length 803;
Best Local Similarity 100.0%; Pred. No. 2.5; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 470 GACTGCTCTCATAGCATCGC 451

RESULT 3
AAH05346/c
ID AAH05346 standard; cDNA; 828 BP.

XX
AC AAH05346;

XX
DT 26-JUN-2001 (first entry)

XX
DE Human cDNA clone (5'-primer) SEQ ID NO:2181.

XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX
OS Homo sapiens.

XX
PN EPI074617-A2.

XX
PD 07-FEB-2001.

XX
PF 28-JUL-2000; 2000EP-00116126.

XX
PR 29-JUN-1999; 99JP-00248036.

XX
PR 27-AUG-1999; 99JP-00300253.

XX
PR 11-JAN-2000; 2000JP-00118776.

XX
PR 02-MAY-2000; 2000JP-00183767.

XX
PR 09-JUN-2000; 2000JP-00241899.

XX
PA (HELI-) HELIX RES INST.

XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Iehli S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.

XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

XX
PS Claim 1; SEQ ID NO 2181; 2537bp + Sequence Listing; English.

XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX length cDNAs defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 14:57:07 ; Search time 41.358 Seconds

(without alignments)
791.274 Million cell updates/sec

Title: US-10-041-856-84

Perfect score: 20

Sequence: 1 gactgctctatgacatgcgc 20

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	3999	US-09-286-891-1	Sequence 1, Appli
C 3	15.4	77.0	2550	US-10-029-180-95	Sequence 95, Appli
C 4	15.4	77.0	5436	US-08-948-277A-2	Sequence 2, Appli
C 5	15.4	77.0	5436	US-09-169-203-2	Sequence 2, Appli
C 6	15.4	77.0	118143	US-09-949-016-17196	Sequence 17196, A
C 7	15.2	76.0	601	US-09-949-016-109435	Sequence 109435,
C 8	15.2	76.0	601	US-09-949-016-109436	Sequence 109436,
C 9	15.2	76.0	24395	US-09-949-016-109437	Sequence 109437,
C 10	15.2	76.0	101835	US-09-949-016-14758	Sequence 14758, A
C 11	15.2	76.0	101835	US-09-949-016-14695	Sequence 14695, A
C 12	15.2	76.0	246444	US-09-949-016-11113	Sequence 13113, A
C 13	14.8	74.0	339	US-09-949-016-1299	Sequence 1290, Ap
C 14	14.8	74.0	601	US-09-949-016-72744	Sequence 72744, A
C 15	14.8	74.0	601	US-09-949-016-89850	Sequence 89850, A
C 16	14.8	74.0	601	US-09-949-016-89851	Sequence 89851, A
C 17	14.8	74.0	601	US-09-949-016-89851	Sequence 89851, A
C 18	14.8	74.0	601	US-09-949-016-89851	Sequence 89851, A
C 19	14.8	74.0	601	US-09-949-016-181156	Sequence 181156,
C 20	14.8	74.0	690	US-09-949-016-183278	Sequence 183278,
C 21	14.8	74.0	8321	US-09-134-000C-1299	Sequence 1299, Ap
C 22	14.8	74.0	9391	US-09-949-016-15013	Sequence 15013, A
C 23	14.8	74.0	15789	US-09-902-540-1139	Sequence 1139, Ap
C 24	14.8	74.0	21513	US-09-949-016-16995	Sequence 16995, A
C 25	14.8	74.0	21513	US-09-949-016-16996	Sequence 16996, A
C 26	14.8	74.0	21513	US-09-949-016-16997	Sequence 16997, A
C 27	14.8	74.0	53789	US-09-949-016-12137	Sequence 12137, A

C 28	14.8	74.0	53789	US-09-949-016-13955	Sequence 13955, A
C 29	14.8	74.0	82000	US-09-949-016-15595	Sequence 15595, A
C 30	14.8	74.0	83665	US-09-949-016-16995	Sequence 16995, A
C 31	14.8	74.0	94077	US-09-949-016-13635	Sequence 13635, A
C 32	14.8	74.0	111677	US-09-949-016-16946	Sequence 16946, A
C 33	14.8	74.0	137394	US-09-949-016-13872	Sequence 13872, A
C 34	14.8	74.0	137743	US-09-949-016-12178	Sequence 12178, A
C 35	14.8	74.0	140925	US-09-949-016-11777	Sequence 11777, A
C 36	14.8	74.0	140982	US-09-949-016-16295	Sequence 16295, A
C 37	14.8	74.0	228896	US-09-949-016-17127	Sequence 17127, A
C 38	14.4	72.0	504	US-09-513-999C-821	Sequence 821, App
C 39	14.4	72.0	518	US-09-221-017B-635	Sequence 635, App
C 40	14.4	72.0	601	US-09-949-016-44914	Sequence 44914, A
C 41	14.4	72.0	601	US-09-949-016-44915	Sequence 44915, A
C 42	14.4	72.0	819	US-09-636-215-571	Sequence 571, App
C 43	14.4	72.0	819	US-09-685-166A-571	Sequence 571, App
C 44	14.4	72.0	819	US-09-679-426-571	Sequence 571, App
C 45	14.4	72.0	819	US-09-759-143-571	Sequence 571, App

ALIGNMENTS

RESULT 1
US-08-971-244-1/c
Sequence 1, Application US/08971244
Patent No. 5891719
GENERAL INFORMATION:
APPLICANT: Cohen, Lucy
APPLICANT: Baerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,244
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3996
US-08-971-244-1
Query Match 100.0%; Score 20; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred. NO. 0.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GACTGCTCTATGACATGC 20
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Db 2478 GACTGCTCTCATGACATCGC 2459

RESULT 2

US-09-286-891-1/c
; Sequence 1, Application US/09286891
; Patent No. 6172195
; GENERAL INFORMATION:
; APPLICANT: Cohen, Lucy
; APPLICANT: Baerle, Patrick
; TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/286,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/971,244
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3996
; US-09-286-891-1

Query Match 100.0%; Score 20; DB 3; Length 3999;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATGACATCGC 20
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Db 2478 GACTGCTCTCATGACATCGC 2459

RESULT 3

US-10-029-180-95
; Sequence 95, Application US/10029180
; Patent No. 6806082
; GENERAL INFORMATION:
; APPLICANT: Call, Brian M.
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin T.
; APPLICANT: Milne, G. Todd
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeffrey C.
; APPLICANT: Trueheart, Josh
; APPLICANT: Zhang, Lixin
; TITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression

; FILE REFERENCE: MIC-004
; CURRENT APPLICATION NUMBER: US/10/029,180
; CURRENT FILING DATE: 2001-12-22
; PRIOR APPLICATION NUMBER: US 60/257,431
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fungal gene
; US-10-029-180-95

Query Match 77.0%; Score 15.4; DB 4; Length 2550;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 878 TGCTCTCATGACATCGC 894

RESULT 4
US-08-948-277A-2
; Sequence 2, Application US/08948277A
; Patent No. 5849581
; GENERAL INFORMATION:
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Zhang, Ning
; TITLE OF INVENTION: Regulators of UCP3 Gene Expression
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,277A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5436 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-948-277A-2

Query Match 77.0%; Score 15.4; DB 2; Length 5436;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTGCTCTCATGACATC 18
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Db 256 ACTGCTCTCATGACATC 272

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 16:38:33 ; Search time 204.198 Seconds
(without alignments)
633.931 Million cell updates/sec

Title: US-10-041-856-84

Perfect score: 20

Sequence: 1 gacgcctcatagcgcgc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues 14575566

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	20	100.0	201	20	US-10-719-993-4509
5	20	100.0	201	20	US-10-719-993-4523
6	20	100.0	201	20	US-10-719-993-4535
7	20	100.0	201	20	US-10-719-993-4536

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c	9	20	100.0	201	20	US-10-719-993-4564	Sequence 4564, Ap
c	10	20	100.0	201	20	US-10-719-993-4565	Sequence 4565, Ap
c	11	20	100.0	201	20	US-10-719-993-4580	Sequence 4580, Ap
c	12	20	100.0	201	20	US-10-719-993-4593	Sequence 4593, Ap
c	13	20	100.0	201	20	US-10-719-993-4594	Sequence 4594, Ap
c	14	20	100.0	201	20	US-10-719-993-4609	Sequence 4609, Ap
c	15	20	100.0	201	20	US-10-719-993-4621	Sequence 4621, Ap
c	16	20	100.0	201	20	US-10-719-993-4622	Sequence 4622, Ap
c	17	20	100.0	201	20	US-10-719-993-34845	Sequence 34845, A
c	18	20	100.0	201	20	US-10-719-993-319	Sequence 319, App
c	19	20	100.0	4256	20	US-09-930-213-276	Sequence 276, App
c	20	20	100.0	4803	21	US-10-956-157-1034	Sequence 1094, Ap
c	21	20	100.0	5840	20	US-10-719-993-322	Sequence 322, App
c	22	20	100.0	5924	13	US-10-041-856-2	Sequence 2, Appl1
c	23	20	100.0	5957	20	US-10-719-993-320	Sequence 320, App
c	24	20	100.0	6107	20	US-10-719-993-321	Sequence 321, App
c	25	20	100.0	6179	20	US-10-719-993-318	Sequence 318, App
c	26	20	100.0	6479	13	US-10-041-856-1	Sequence 1, Appl1
c	27	20	100.0	78878	20	US-10-719-993-6863	Sequence 6863, Ap
c	28	20	100.0	82.0	25	US-10-719-956-141010	Sequence 141010,
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c	31	15.8	79.0	405	9	US-09-795-668-1453	Sequence 1453, Ap
c	32	15.8	79.0	405	9	US-09-946-807-1453	Sequence 1453, Ap
c	33	15.8	79.0	435	19	US-10-437-963-43775	Sequence 43775, A
c	34	15.8	79.0	587	13	US-10-027-632-39553	Sequence 39553, A
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c	36	15.8	79.0	587	13	US-10-027-632-314336	Sequence 314336, A
c	37	15.8	79.0	587	17	US-10-027-632-39553	Sequence 39553, A
c	38	15.8	79.0	587	17	US-10-027-632-314335	Sequence 314335, A
c	39	15.8	79.0	587	17	US-10-027-632-314336	Sequence 314336, A
c	40	15.8	79.0	1016	19	US-10-437-963-30748	Sequence 30748, A
c	41	15.8	79.0	29844	21	US-10-468-326-3	Sequence 3, Appl1
c	42	15.8	79.0	51615	13	US-10-087-192-1972	Sequence 1972, Ap
c	43	15.8	79.0	81924	19	US-10-741-601-5636	Sequence 5636, Ap
c	44	15.8	79.0	180227	19	US-10-322-681-308	Sequence 308, App
c	45	15.8	79.0	1503841	9	US-09-795-668-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-10-041-856-84
; Sequence 84, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES P.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041, 856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-041-856-84

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. NO. 2.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACTGCTCTCATAGCCTGC 20
|||||

Db 1 GACTGCTCTCATAGCATCGC 20

RESULT 2

US-10-719-993-4494/c
; Sequence 4494, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4494
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4494

Query Match 100.0%; Score 20; DB 20; Length 201;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATAGCATCGC 20

Db 34 GACTGCTCTCATAGCATCGC 15

RESULT 3

US-10-719-993-4508/c
; Sequence 4508, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4508
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4508

Query Match 100.0%; Score 20; DB 20; Length 201;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATAGCATCGC 20

Db 133 GACTGCTCTCATAGCATCGC 114

RESULT 4

US-10-719-993-4509/c
; Sequence 4509, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4509

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-719-993-4509

Query Match 100.0%; Score 20; DB 20; Length 201;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATAGCATCGC 20

Db 89 GACTGCTCTCATAGCATCGC 70

RESULT 5

US-10-719-993-4523/c
; Sequence 4523, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4523
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4523

Query Match 100.0%; Score 20; DB 20; Length 201;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATAGCATCGC 20

Db 34 GACTGCTCTCATAGCATCGC 15

RESULT 6

US-10-719-993-4535/c
; Sequence 4535, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CU001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4535
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-4535

Query Match 100.0%; Score 20; DB 20; Length 201;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATAGCATCGC 20

Db 133 GACTGCTCTCATAGCATCGC 114

RESULT 7

US-10-719-993-4536/c
; Sequence 4536, Application US/10719993

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 15:46:58 ; Search time 979.383 Seconds
(without alignments)
777.311 Million cell updates/sec

Title: US-10-041-856-84

Perfect score: 20
Sequence: 1 gactgcctcatagcaccgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hrc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_g881:
9: gb_g882:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	231	7	N56173 J8210F Huma
2	20	100.0	258	7	Z42212 HSC0CD041 n
3	20	100.0	380	7	CR788009 DKFZp459M
4	20	100.0	492	7	H15327 ym28d08.t1
5	20	100.0	529	1	AU127237
6	20	100.0	550	6	CA397687 cs94d05.Y
7	20	100.0	568	7	AM246917 2822633.5
8	20	100.0	583	5	BP311692 BP311692
9	20	100.0	603	5	BK478139 DKFZp686B
10	20	100.0	766	7	CR789373 DKFZp459J
11	20	100.0	793	1	CN256150 170005318
12	20	100.0	803	7	AU124100 AU124100
13	20	100.0	828	1	AU124187
14	20	100.0	849	5	AU935143 AGENCOURT
15	20	100.0	853	7	CF552514 AGENCOURT
16	20	100.0	866	5	BU508979 AGENCOURT
17	20	100.0	868	5	BU508979 AGENCOURT
18	20	100.0	874	5	BU5156074
19	20	100.0	885	5	BQ428500 AGENCOURT
20	20	100.0	887	5	BU849172 AGENCOURT
21	20	100.0	906	5	BU554148 AGENCOURT
22	20	100.0	923	5	BU147179 AGENCOURT
23	20	100.0	931	4	BG286503 6023822955
24	20	100.0	937	2	BE893879 601436245

25	20	100.0	945	5	BU845774	BU845774 AGENCOURT
26	20	100.0	1000	4	BM471267	BM471267 AGENCOURT
27	20	100.0	3833	3	CR749385	CR749385 Homo sapi
28	20	100.0	3999	9	AY414501	AY414501 Homo sapi
29	20	100.0	3999	9	AY414502	AY414502 Pan trogl
30	18.4	92.0	641	5	BQ807986	BQ807986 NISC_KR12
31	18.4	92.0	1134	7	CN641971	CN641971 ILLUMIGEN
32	18	90.0	1458	9	CU105854	CU105854 ISB1-45M8
33	17.4	87.0	970	8	CC405446	CC405446 PNH0J22TD
34	17	85.0	818	7	CF752151	CF752151 OM_R000.6
35	16.8	84.0	168	7	CV402642	CV402642 RC0-BN023
36	16.8	84.0	171	9	BX572126	BX572126 Arabidops
37	16.8	84.0	256	5	BU715404	BU715404 SUMCAB03
38	16.8	84.0	471	2	AW593718	AW593718 hg21e08.x
39	16.8	84.0	555	2	BF582892	BF582892 602101339
40	16.8	84.0	558	4	BG964036	BG964036 602828778
41	16.8	84.0	560	2	BF577636	BF577636 602092511
42	16.8	84.0	560	2	BF584731	BF584731 602098479
43	16.8	84.0	565	2	BF581514	BF581514 602101032
44	16.8	84.0	569	4	BG964537	BG964537 602832213
45	16.8	84.0	577	2	BF583651	BF583651 602101442

ALIGNMENTS

RESULT 1
LOCUS N56173 231 bp mRNA linear EST 20-FEB-1996
DEFINITION J8210F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA
clone J8210 5', mRNA sequence.

ACCESSION N56173
VERSION N56173.1 GI:1199021
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE Liew,C.C.
CDNAs from fetal heart
Unpublished (1995)
JOURNAL Contact: Liew CC
COMMENT Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cllw@rics.bwh.harvard.edu
Seq primer: TCCAAAGATTGGCAGCAG.

FEATURES

source location/Qualifiers
1..231
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="J8210"
/lab_host="E. coli XL1-Blue"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). CDNA was synthesized using a XhoI-Oligo dt
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 231;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGCTCTCATACATCGC 20
|||||
DB 144 GACTGCTCTCATACATCGC 125

RESULT 2
 242212/c
LOCUS
DEFINITION HSC0CD041 normalized infant brain cDNA Homo sapiens CDNA clone
ACCESSION 242212
VERSION 242212.1
KEYWORDS GI:565316
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 258)
AUTHORS Auffray, C., Behar, G., Boie, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pietu, G., Pouliot, Y., Sbaastiani-Kabatchis, C. and Tessier, A.
TITLE IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 952757534
PUBMED 7757816
COMMENT Contact: Genethon
 Genexpress-Genethon
 Genethon Centre de recherche sur le Genome Humain
 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
 Tel: 33169472800
 Fax: 33160778698
 Email: genexpress@genethon.fr
 Single read.
 Genexpress library id: C; Genexpress_sequence_id: Y1C-0cd04
 Seq primer: (-21)M3 universal.
FEATURES
 source
 location/Qualifiers
 1..258
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C-0cd04"
 /sex="Female"
 /tissue_type="total brain"
 /dev_stage="3 months old"
 /clone_lib="normalized infant brain cDNA"
 /note="Organ: brain; Vector: lafmid BA; Site 1: HindIII; Site 2: NotI; sex:Female; dev stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
ORIGIN
 Query Match 100.0%; Score 20; DB 7; Length 258;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GACTGCTCTCATGATCGC 20
 ||||||||||||||||||||
 Db 205 GACTGCTCTCATGATCGC 186
RESULT 3
 CR788009/c
LOCUS
DEFINITION DKFZp459M2022_r1 459 (synonym: pcor1) Pongo pygmaeus CDNA clone
ACCESSION CR788009
VERSION CR788009.1
KEYWORDS GI:53707006
SOURCE EST.
ORGANISM Pongo pygmaeus (orangutan)

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo. 1 (bases 1 to 380)
AUTHORS Ottenwaelder, B., Obermaier, B., Deuschle, S., Schaidp, A., Mewes, H.W., Weill, B., Amid, C., Oeanger, A., Fodor, G., Han, M. and Wiemann, S.
TITLE Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B., Deuschle, S., et al.)
JOURNAL Deutscher, S., et al.)
COMMENT Unpublished (2004)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann, This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Mariner/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp459M2022) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459M2022
 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
FEATURES
 source
 location/Qualifiers
 1..380
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp459M2022"
 /tissue_type="cortex"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="459 (synonym: pcor1)"
 /note="Vector: pSPORT1_sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN
 Query Match 100.0%; Score 20; DB 7; Length 380;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GACTGCTCTCATGATCGC 20
 ||||||||||||||||||||
 Db 294 GACTGCTCTCATGATCGC 275
RESULT 4
 H15327/c
LOCUS
DEFINITION YN2808.r1 Soares infant brain INIB Homo sapiens CDNA clone
ACCESSION H15327
VERSION H15327.1
KEYWORDS GI:880147
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 492)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 2471
 High quality sequence steps: 367
 Source: IMAGE Consortium, LNL